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(21) International Application Number: PCT/AU98/00564 (22) International Filing Date: 17 July 1998 (17.07.98) (30) Priority Data: PO 8117 18 July 1997 (18.07.97) AU (71) Applicant (for all designated States except US): THE UNIVERSITY OF SYDNEY [AU/AU]; Parramatta Road, Sydney, NSW 2006 (AU). (72) Inventor; and (75) Inventor/Applicant (for US only): WEISS, Anthony, Steven [AU/AU]; 235 Rainbow Street, Randwick, NSW 2031 (AU). (74) Agent: GRIFFITH HACK; G.P.O. Box 4164, Sydney, NSW 2001 (AU).			(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i>
(54) Title: TROPOELASTIN DERIVATIVES			
(57) Abstract <p>The invention relates to derivatives of tropoelastin and variants of those derivatives. The invention further provides expression products and hybrid molecules of the derivatives and variants of the invention. The invention further provides methods for the production of the derivatives, variants, expression products and hybrid molecules. Further provided are formulations, cross-linked structures and implants comprising the derivatives, variants, expression products and hybrid molecules of the invention. Further provided are uses of the derivatives, variants, expression products and hybrid molecules of the invention.</p>			

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TROPOELASTIN DERIVATIVES

TECHNICAL FIELD

The present invention relates to derivatives of human
5 tropoelastin and variants thereof, to genetic constructs
encoding the amino acid sequences of the derivatives and
variants and to uses of the derivatives and variants. In
particular, the derivatives of the present invention have
10 elastin-like properties or macro-molecular binding
properties.

BACKGROUND ART

There are various forms of tropoelastin that
typically appear to consist of two types of alternating
15 domains: those rich in hydrophobic amino acids
(responsible for the elastic properties) and those rich in
lysine residues (responsible for cross-link formation).
Hydrophobic and cross-linking domains are encoded in
separate exons (Indik *et al* 1987).

20 The 26 A region of human tropoelastin is unique
amongst tropoelastin domains in that, due to the absence
of lysine, this region does not participate in elastin
cross-link formation. Furthermore, this region is a
serine-rich domain and lacks hydrophobic stretches,
25 indicating that it is unlikely to contribute to the
elasticity of tropoelastin. There is otherwise limited
information on the structure and functional relationships
of the 26 A region (Bedell-Hogan *et al.*, 1993).

The gene for tropoelastin is believed to be present
30 as a single copy in the mammalian genome, and is expressed
in the form of multiple transcripts, distinguished by
alternative splicing of the pre-mRNA (Indik *et al*, 1990;
Oliver *et al*, 1987). Modest expression of a natural human
tropoelastin sequence has been achieved by Indik *et al*
35 (1990) using cDNA, providing free polypeptide which
unfortunately was unstable.

Expression of substantial amounts of human
tropoelastin using synthetic polynucleotides is reported

in WO94/14958. In particular, a construct, SHEL, providing substantial amounts of full length human tropoelastin is described.

5

DESCRIPTION OF THE INVENTION

In the specification and claims, "derivatives of human tropoelastin" or "tropoelastin derivatives" means novel peptides, polypeptides or proteins which contain amino acid sequences derived from the native amino acid sequences of human tropoelastin molecules. The amino acid sequences of the derivatives of human tropoelastin may be derived from any of the amino acid sequences of the isoforms of human tropoelastin. Derivatives of human tropoelastin are distinguished from human tropoelastin molecules in that the amino acid sequences of derivatives are altered with respect to native tropoelastin sequences by substitution, addition or deletion of residues, or a combination of these alterations, in derivative amino acid sequences.

20 In a first aspect, the present invention provides derivatives of human tropoelastin which have elastin-like properties. Elastin-like properties are a combination of elastic properties, including the phenomenon of recoil following molecular distention under appropriate conditions, and the ability to be cross-linked to other elastin molecules and/or other elastin-like molecules.

25 In a second aspect, the present invention provides derivatives of human tropoelastin which have macro-molecular binding properties including the ability to bind glycosaminoglycans.

30 In a third aspect, the present invention provides derivatives of human tropoelastin which have elastin-like properties and macro-molecular binding properties.

35 The present invention further provides amino acid sequence variants of the derivatives of the invention. In the specification and claims "variants" means amino acid sequences which retain the properties of the corresponding derivative of human tropoelastin, for example, elastin-

like properties or macro-molecular binding properties, or a combination of elastin-like properties and macro-molecular binding properties, and have an amino acid sequence which is homologous with the amino acid sequence of the corresponding derivative. For the purposes of this description, "homology" between the amino acid sequence of a particular derivative of human tropoelastin and another amino acid sequence connotes a likeness short of identity, indicative of a derivation of one sequence from the other. In particular, an amino acid sequence is homologous to a derivative of human tropoelastin if the alignment of that amino acid sequence with the sequence of the derivative of human tropoelastin reveals a similarity of about 65% over any 20 amino acid stretch or over any repetitive element of the molecules shorter than 20 amino acids in length. Such a sequence comparison can be performed via known algorithms, such as that of Lipman and Pearson (1985). Similarity is observed between amino acids where those amino acids have a side chain which confers a similar chemical property in the same chemical environment. For example, threonine and serine are similar amino acids; aspartic acid and glutamic acid are similar amino acids; valine, leucine and isoleucine are similar amino acids etc. Thus, an amino acid sequence may be considered homologous with the amino acid sequence of a human tropoelastin derivative because the alignment of those sequences reveals a similarity of 65%, although at each amino acid position in the aligned sequences, none of the residues are identical.

Inasmuch as the present invention provides derivatives of human tropoelastin and amino acid sequence variants of those derivatives, the invention thus extends to amino acid sequence variants incorporating amino acid sequences of non-human tropoelastins. Amino acid sequence variants which are non-human tropoelastin derivatives, or are based all, or in part, on non-human tropoelastin derivatives retain properties of the corresponding derivative of non-human tropoelastin, for example,

elastin-like properties or macro-molecular binding properties, or a combination of elastin-like properties and macro-molecular binding properties, and have an amino acid sequence which is homologous with the amino acid sequence of the corresponding human derivative. The variants of the invention also include variants of the non-human tropoelastin derivatives, or of derivatives based on the non-human tropoelastin derivatives.

"Homology" between the amino acid sequence of a particular derivative of non-human tropoelastin and another amino acid sequence connotes a likeness short of identity, indicative of a derivation of one sequence from the other. In particular, an amino acid sequence is homologous to a derivative of non-human tropoelastin if the alignment of that amino acid sequence with the sequence of the derivative of non-human tropoelastin reveals a similarity of about 65% over any 20 amino acid stretch or over any repetitive element of the molecules shorter than 20 amino acids in length. The skilled addressee will understand that species that are substantially phylogenetically related to humans express tropoelastin molecules which consist of amino acid sequences with homology to human tropoelastin amino acid sequences. Indeed, amino acid sequences of non-human tropoelastins have been determined, including the amino acid sequences of chick tropoelastin, bovine tropoelastin and rat tropoelastin (Bressan et al. 1987, Raju et al. 1987, Pierce et al. 1992) and over multiple regions, these are homologous with the human tropoelastin amino acid sequences. The skilled addressee will recognise therefore, that derivatives of human tropoelastin and amino acid sequence variants of those derivatives will necessarily encompass corresponding tropoelastin amino acid sequences from these and other non-human species.

The present invention provides a tropoelastin derivative comprising the amino acid sequence of SHELδmodified (SEQ ID NO:5). The amino acid sequence of

SHELδmodified and the alignment of that amino acid sequence with the human tropoelastin sequence is shown in Figure 5.

The invention also provides an amino acid sequence
5 variant of the derivative comprising the amino acid sequence of SHELδmodified.

The invention also provides a polynucleotide encoding a tropoelastin derivative comprising the amino acid sequence of SHELδmodified. The nucleotide sequence
10 encoding SHELδmodified is shown in Figure 3 (SEQ ID NO: 4). Preferably the polynucleotide comprises the nucleotide sequence which corresponds to SHELδmodified shown in Figure 3.

The invention also provides a polynucleotide encoding
15 an amino acid sequence variant of the derivative SHELδmodified.

The present invention further provides a synthetic polynucleotide encoding a tropoelastin derivative comprising the amino acid sequence of SHELδ26A (SEQ ID
20 NO:3). A synthetic polynucleotide is a molecule which comprises a nucleotide sequence that contains silent mutations with respect to the corresponding native polynucleotide molecule. The silent mutations enhance the expression of the synthetic polynucleotide. The amino
25 acid sequence of SHELδ26A and the alignment of that amino acid sequence with the human tropoelastin sequence is shown in Figure 2. The SHELδ26A derivative excludes the SHEL coding sequence corresponding to exon 26A. Preferably the synthetic polynucleotide comprises the
30 sequence shown in Figure 1 (SEQ ID NO:1) from nucleotide position 1 to 1676 contiguous with nucleotide position 1775 to 2210.

The invention also provides a polynucleotide encoding an amino acid sequence variant of the derivative SHELδ26A.

35 The invention also provides an amino acid sequence

variant of the derivative comprising the amino acid sequence of SHEL826A.

5 The present inventor has, for the first time, shown that the region encoded by exon 26A (peptide 26A) of the tropoelastin gene binds glycosaminoglycans (GAGs) (Figure 6A and B). GAGs are macro-molecules particularly associated with the extracellular environment. These molecules play an important role in the architecture and mechanical properties of connective tissues and mediate
10 interactions with and availability of other molecules.

Thus, the present invention provides a tropoelastin derivative comprising the amino acid sequence of peptide 26A. Peptide 26A has the amino acid sequence:
GADEGVRRSLSPELREGDPSSSQHLPSTPSSPRV (SEQ ID NO: 12) or
15 GADEGVRRSLSPELREGDPSSSQHLPSTPSSPRF (SEQ ID NO: 13).

The present invention also provides an amino acid sequence variant of the derivative comprising the amino acid sequence of peptide 26A.

The invention also provides a polynucleotide encoding
20 a tropoelastin derivative comprising the amino acid sequence of peptide 26A. Preferably the polynucleotide comprises the nucleotide sequence shown in Figure 1 (SEQ ID NO: 1) from nucleotide position 1687 to 1778. Preferably the 3' terminal codon is GTT (which encodes V)
25 or TTT (which encodes F).

The invention also provides a polynucleotide encoding an amino acid sequence variant of the derivative comprising the amino acid sequence of peptide 26A.

In appreciating the GAG binding property of peptide
30 26A, the present inventor envisages the generation of novel subsets of hybrid molecules, comprising biological polymers which are linked to peptide 26A, wherein the peptide 26A imparts GAG binding activity to the polymer. In particular, the present inventor has recognised that
35 the deletion or insertion of the peptide 26A amino acid sequence, or a variant of that amino acid sequence will alter GAG binding activity. Thus, the present invention relates to tropoelastin derivatives in which full length

or partial length tropoelastin molecules have been modified by the addition of one or more exon 26A regions to enhance interactions with GAGs. Moreover, the invention relates to site directed modification of the amino acid sequence of peptide 26A so as to generate variants of the peptide 26A amino acid sequence which have altered affinity or altered specificity for GAGs. Tropoelastin derivatives or variants of the derivatives which contain altered GAG binding activity may be uncross-linked or cross-linked.

In another aspect, the invention provides a hybrid molecule. In the specification and claims, "hybrid molecule" means a molecule comprising a biological polymer which is linked to a tropoelastin derivative comprising the amino acid sequence of peptide 26A or an amino acid sequence variant of a derivative comprising the amino acid sequence of peptide 26A. Preferably the biological polymer is a protein. More preferably the protein is selected from the group consisting of growth factors, cytokines and antibodies. Alternatively the biological polymer is selected from the group consisting of lipids, sugars or nucleic acids.

In one embodiment, and where the biological polymer is a protein, the hybrid molecule is produced by recombinant DNA techniques, including for example the construction of a nucleotide sequence which encodes the biological polymer and the tropoelastin derivative comprising the amino acid sequence of peptide 26A, or the amino acid sequence variant of a derivative comprising the amino acid sequence of peptide 26 A, in a single open reading frame. Alternatively, the hybrid molecule may be produced synthetically by solid phase peptide synthesis, including, for example the methods of synthesis disclosed in Merrifield (1963) or Knorr et al. (1989). Examples of peptide synthesis also include the synthesis methods used by peptide synthesizers of Perkin Elmer/Applied Biosystems, CA, US.

In another aspect, the invention provides a

polynucleotide sequence encoding a hybrid molecule of the invention.

In another aspect, the invention provides a hybrid molecule which comprises a synthetic polymer which is
5 linked in a tropoelastin derivative comprising the amino acid sequence of peptide 26A, or an amino acid sequence variant of the derivative comprising the amino acid sequence of peptide 26A.

The invention further provides a method of imparting
10 or enhancing GAG binding activity to a biological polymer comprising the step of linking a tropoelastin derivative comprising the amino acid sequence of peptide 26A, or an amino acid sequence variant of peptide 26A with the biological polymer. Preferably the biological polymer is
15 a protein.

The invention further provides a method of deleting or reducing GAG binding activity from a biological polymer comprising the step of deleting a tropoelastin derivative comprising the amino acid sequence of peptide 26A, or an
20 amino acid sequence variant of peptide 26A from the biological polymer. Preferably the biological polymer is a protein.

The present invention also provides a tropoelastin derivative comprising the amino acid sequence of
25 SHELgamma. SHELgamma has the amino acid sequence:
SANGALVGLGVPGGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPR
VPGALAAAKAAKYGA AVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAKAAKAAQFG
LVGAAGLGGGLGVGGLGVPGVGGLGGIPPAKAAKYGAAGLGGVLGGAGQFPLGGVA
ARPGFGLSPIFPGGACLGKACGRKRK (SEQ ID NO: 9).

30 The invention also provides an amino acid sequence variant of the derivative comprising the amino acid sequence of SHELgamma.

The invention also provides a polynucleotide encoding a tropoelastin derivative, the derivative comprising the
35 amino acid sequence of SHELgamma. The nucleotide sequence of the polynucleotide SHELgamma (SEQ ID NO: 8) is shown in Figure 8. In this nucleotide sequence, the first 9 codons from nucleotide position 948 to 974 are derived

from the glutathione *S*-transferase (GST) fusion nucleotide sequence. Preferably the polynucleotide comprises the nucleotide sequence shown in Figure 8. More preferably the polynucleotide comprises the nucleotide sequence shown in Figure 8 from nucleotide sequence position 975 to 1547.

The invention also provides a polynucleotide encoding an amino acid sequence variant of the derivative comprising the amino acid sequence of SHELgamma.

The present invention also provides a polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHELgamma excluding exon 26A. The nucleotide sequence of the polynucleotide SHELgamma excluding exon 26A (SEQ ID NO: 6) is shown in Figure 7. In this nucleotide sequence, the first 5 codons from nucleotide position 948 to 962 are derived from the GST nucleotide sequence. SHELgamma excluding exon 26A has the following amino acid sequence:

VP GALAAAKA AKYGA AVPGVLGGLGALGGVGVIPGGVVGAGPAAAAAKAAAKAAQFG
LVGAAGLGGLGVGGLGVPGVGGGLGGIPPAAKA AKYGAAGLGGVLGGAGQFPLGGVA
ARPGFGLSPIFPGGACLGKACGRKRK (SEQ ID NO: 7).

Preferably the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 6. More preferably the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 6 from nucleotide sequence position 15 to 441.

The invention also provides a polynucleotide encoding an amino acid sequence variant of the derivative comprising the amino acid sequence of SHELgamma excluding exon 26A.

The invention also provides a tropoelastin derivative comprising the amino acid sequence of SHELgamma excluding exon 26A.

The invention also provides an amino acid sequence variant of the derivative comprising SHELgamma excluding exon 26A.

The derivatives of the invention based on SHELgamma can also be produced by *in vitro* biochemical cleavage of tropoelastin products such as SHEL, so as to release a carboxy-terminal fragment. The carboxy-terminal fragment

may be purified by reverse phase HPLC.

The present invention also provides a tropoelastin derivative comprising the amino acid sequence of SHEL31-36. SHEL31-36 has the following amino acid sequence:

5 GIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACG-RKRK (SEQ ID NO: 10).

SHEL31-36 retains a crosslinking domain. As a consequence of its elastin-like properties, it is envisaged that this and related tropoelastin derivatives
10 can be used to interfere with tropoelastin deposition and formation of unaltered elastic fibre.

The invention also provides an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL31-36.

15 The invention also provides a polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHEL31-36. Preferably the polynucleotide comprises the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) from nucleotide position 2022 to
20 2210.

The invention also provides a polynucleotide encoding an amino acid variant of the derivative comprising the amino acid sequence of SHEL31-36.

The present invention also provides a tropoelastin
25 derivative, comprising the amino acid sequence of SHEL32-36. SHEL32-36 has the following amino acid sequence: GAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK (SEQ ID NO: 11).

The invention also provides an amino acid sequence
30 variant of the derivative comprising the amino acid sequence of SHEL32-36.

The invention also provides a polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHEL32-36. Preferably the
35 polynucleotide comprises the nucleotide sequence shown in Figure 1 (SEQ ID NO: 1) from nucleotide position 2061 to 2210.

The present invention also provides a polynucleotide

encoding an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL32-36.

As a consequence of its elastin-like properties, it is envisaged that SHEL32-36 and related tropoelastin derivatives can be used to interfere with tropoelastin deposition and formation of an unaltered elastic fibre.

The present invention also provides a tropoelastin derivative, comprising the amino acid sequence of SHEL26-36. SHEL26-36 has the following amino acid sequence:

10 AAAGLGAGIPGLGVGVGPGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGD
PSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAA
AAAKAAAKAAQFGLVGAAGLGGLVGGLGVPGVGGGLGGIPPAATAAKAAKYGAAGLGGV
LGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK (SEQ ID NO: 14)

The invention also provides an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL26-36.

The invention also provides a polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHEL26-36. Preferably the polynucleotide comprises the nucleotide sequence shown in Figure 1 from nucleotide position 1554-2210.

The present invention also provides a tropoelastin derivative, comprising the amino acid sequence of SHEL26-36 excluding exon 26A. SHEL26-36 excluding exon 26A has the following amino acid sequence:

25 AAAGLGAGIPGLGVGVGPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVP
GVLGGLGALGGVGIPGGVVGAGPAAAAAAKAAKAAQFGLVGAAGLGGLVGGLGVPG
VGGLGGIPPAATAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGK
ACGRKRK (SEQ ID NO: 15)

The invention also provides an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL26-36 excluding exon 26A.

The invention also provides a polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHEL26-36 excluding exon 26A. Preferably the polynucleotide comprises the nucleotide sequence shown in Figure 1 from nucleotide position 1554

to 1676 contiguous with 1776 to 2210.

The present invention also provides a polynucleotide encoding an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL26-36.

5 In another aspect the present invention provides a formulation comprising a tropoelastin derivative, a variant of the derivative or a hybrid molecule of the invention, together with a carrier or diluent.

10 Formulations of the derivatives, variants or hybrid molecules of the invention can be prepared in accordance with standard techniques appropriate to the field in which they are to be used.

15 The polynucleotides and synthetic polynucleotides of the invention can be provided in association with other polynucleotide sequences including 5' and 3' untranslated sequences, and 5' upstream and 3' downstream transcriptional regulatory sequences. The polynucleotides and synthetic polynucleotides may be provided as a recombinant DNA molecule including plasmid DNA.

20 The polynucleotides and synthetic polynucleotides of the invention can be prepared using the techniques of chemical synthesis or recombinant DNA technology, or by a combination of both techniques.

25 In a further aspect the invention provides a vector comprising a polynucleotide or synthetic polynucleotide encoding a tropoelastin derivative, a variant of the derivative or a hybrid molecule of the invention.

30 Vectors useful in this invention include plasmids, phages and phagemids. The polynucleotides and synthetic polynucleotides of the present invention can also be used in integrative expression systems or lytic or comparable expression systems.

35 Suitable vectors will generally contain origins of replication and control sequences which are derived from species compatible with the intended expression host. Typically these vectors include a promoter located upstream from the polynucleotide, together with a ribosome binding site if intended for prokaryotic expression, and a

phenotypic selection gene such as one conferring antibiotic resistance or supplying an auxotrophic requirement. For production vectors, vectors which provide for enhanced stability through partitioning may be
5 chosen. Where integrative vectors are used it is not necessary for the vector to have an origin of replication. Lytic and other comparable expression systems do not need to have those functions required for maintenance of vectors in hosts.

10 For *E. coli* typical vectors include pBR322, pBluescript II SK⁺, pGEX-2T, pTrc99A, pET series vectors, particularly pET3d, (Studier et al., 1990) and derivatives of these vectors. Derivatives include those plasmids with a modified protease recognition sequence to facilitate
15 purification of a protein domain.

In another aspect the invention provides a cell capable of expressing a polynucleotide or a synthetic polynucleotide which encodes a derivative or variant of the invention, or a polynucleotide which encodes a hybrid
20 molecule of the invention.

A preferred expression system is an *E. coli* expression system. However, the invention includes within its scope the use of other hosts capable of expressing protein from the polynucleotides designed for use in *E.*
25 *coli*. The invention also includes the use of polynucleotides and synthetic polynucleotides suitable for use in other expression systems such as other microbial expression systems. These other expression systems include yeast, and bacterial expression systems, insect
30 cell expression systems, and expression systems involving other eukaryotic cell lines or whole organisms.

Examples of *E. coli* hosts include *E. coli* B strain derivatives (Studier et al., 1990), and K-strain derivatives such as NM522 (Gough and Murray, 1983) and
35 XL1-Blue (Bullock et al., 1987).

In a further aspect the present invention provides an expression product. In the specification and claims, "expression product" means a derivative or variant of the

invention expressed by a cell containing a polynucleotide or a synthetic polynucleotide encoding a derivative or variant of the invention.

5 The expression products of the invention may be fused expression products which include all or part of a protein encoded by the vector in peptide linkage with the derivative or variant. They may also include, for example, an N-terminal methionine or other additional residues which do not permanently impair the elastin-like, 10 or macro-molecular binding properties of the product.

Typically the fusion is to the N-terminus of the expression product. An example of a suitable protein is to the C-terminus of glutathione *S*-transferase. The fused protein sequence may be chosen in order to cause the 15 expression product to be secreted or expressed as a cell surface protein to simplify purification or expressed as a cytoplasmic protein.

The expressed fusion products may subsequently be treated to remove the fused protein sequences to provide 20 free tropoelastin derivative or variant. Treatment is typically through protease treatment or, in the case of secretion, removal is effected by endogenous host secretion machinery. An example of this is secretion by yeasts.

25 Non-fused systems include the introduction of or use of a pre-existing methionine codon. An example of this is the use of pET3a or pET3d in *E. coli*.

In another aspect the invention provides a polynucleotide encoding an expression product of the 30 invention.

In another aspect the present invention provides a formulation comprising an expression product of the invention together with a carrier or diluent. The formulation of the expression product can be prepared in 35 accordance with standard techniques appropriate to the field in which they are to be used.

According to a further aspect of the present invention there is provided a method for producing a

tropoelastin derivative or a variant of the derivative comprising providing a vector containing a polynucleotide or a synthetic polynucleotide encoding the derivative or variant; introducing the vector into a suitable host cell; maintaining the cell in conditions suitable for expression of the polynucleotide or synthetic polynucleotide and isolating the derivative or variant of the invention. The method can be applied to the production of the expression products and hybrid molecules (in which the hybrid molecules comprise the peptide 26A or a variant thereof and a further amino acid sequence) of the invention, by providing a vector containing a polynucleotide encoding an expression product or a hybrid molecule; introducing the vector into a suitable host cell; maintaining the cell in conditions suitable for expression of the polynucleotide and isolating the expression product or hybrid molecule.

In one embodiment, the polynucleotide or synthetic polynucleotide encoding the derivative, variant, expression product or hybrid molecule of the invention is expressed in a host cell which is maintained in culture *in vitro*.

Alternatively, the polynucleotide or synthetic polynucleotide encoding the derivative, variant, expression product or hybrid molecule of the invention is expressed in a host cell which is maintained *in vivo*. Thus, in another embodiment, the polynucleotide or synthetic polynucleotide encoding the derivative, variant, expression product or hybrid molecule of the invention is expressed in a transgenic animal. Methods for the generation of transgenic animals are known in the art. Exemplary methods are described in Slack et al. 1991 and Janne et al. 1992.

The tropoelastin derivatives, variants of the derivatives, and hybrid molecules (in which the hybrid molecules comprise the peptide 26A or a variant thereof and a further amino acid sequence) of the invention may be produced by solid phase peptide synthesis, including, for example, the methods of synthesis disclosed in Merrifield

(1963) or Knorr et al (1989). Examples of peptide synthesis also include the synthesis methods used by peptide synthesizers of Perkin Elmer/Applied Biosystems, CA, US. As an alternative to cell synthesis from a polynucleotide or synthetic polynucleotide, the expression products of the invention may be produced by solid phase peptide synthesis.

In a further aspect the present invention provides an implant formed from at least one tropoelastin derivative and/or variant of the derivative of the invention. The implant may alternatively contain at least one expression product and/or at least one hybrid molecule of the invention.

The implants are formed into the required shape by cross-linking the tropoelastin derivative, variant of the derivative, expression product, or hybrid molecule of the invention, in a mould which conforms to the desired shape of the implant. Where the implant is required to be used in sheet form the tropoelastin derivative, variant of the derivative, expression product, or hybrid molecule of the invention can be cross-linked on a flat surface. Relevant methodologies are described in, for example, US Patent No. 4 474 851 and US Patent No. 5 250 516. The elastomeric materials may be exclusively prepared from one or more tropoelastin derivatives, variants of the derivative, expression products, or hybrid molecules of the invention or may be composites prepared from one or more of these constituents together with other materials.

The tropoelastin derivatives or variants of the derivatives can be cross-linked to form elastin or elastin-like material or can be cross-linked in conjunction with other biological or synthetic molecules to form a composite material.

Thus in another aspect the invention provides a cross-linked complex which comprises at least one tropoelastin derivative of the invention and/or at least one variant of a derivative of the invention. The cross-linked complexes may additionally contain at least one

expression product and/or at least one hybrid molecule of the invention, which may be cross-linked to the at least one tropoelastin derivative and/or variant of the derivative of the invention.

5 The cross-linking of the tropoelastin derivatives, variants of the derivatives, hybrid molecules and expression products of the invention can be achieved by chemical oxidation of lysine side chains using processes such as ruthenium tetroxide mediated oxidation and quinone
10 mediated oxidation, or by using homobifunctional chemical cross-linking agents such as dithiobis (succinimidylpropionate), dimethyl adipimidate or dimethyl pimelimidate. Glutaraldehyde cross-linking is an important addition to this repertoire. Another alternative
15 is the cross-linking of lysine and glutamic side chains.

 The tropoelastin derivatives, variants of the derivatives, hybrid molecules and expression products of the invention may also be enzymatically cross-linked by methods including lysyl oxidase mediated oxidation or may
20 be cross-linked using gamma irradiation.

BRIEF DESCRIPTION OF THE DRAWINGS

 Figure 1: Nucleotide (SEQ ID NO: 1) and predicted amino acid (SEQ ID NO:2) sequences of synthetic human
25 tropoelastin SHEL. The upper (numbered) nucleotide sequence represents the coding strand.

 Figure 2: Alignment of SHEL (SEQ ID NO:2) (upper line) and SHEL δ 26A (SEQ ID NO: 3) amino acid sequences.

 Figure 3: Nucleotide (SEQ ID NO: 4) and predicted
30 amino acid (SEQ ID NO: 5) sequences of SHEL δ modified.

 Figure 4: Alignment of SHEL δ modified (SEQ ID NO: 4) (upper line) and SHEL (SEQ ID NO:1) nucleotide sequences.

 Figure 5: Alignment of SHEL δ modified (SEQ ID NO: 5) (lower line) and SHEL (SEQ ID NO: 1) amino acid
35 sequences.

 Figure 6A: HPLC elution profile of GST-exon 26A fusion protein tropoelastin derivative loaded in from

heparin sepharose. 6B: Binding of peptide 26A (SEQ ID NO: 12 and SEQ ID NO: 13) to glycosaminoglycans.

Figure 7: Nucleotide (SEQ ID NO: 6) and predicted amino acid (SEQ ID NO: 7) sequences of SHELgamma excluding
5 exon 26A.

Figure 8: Nucleotide (SEQ ID NO: 8) and predicted amino acid (SEQ ID NO: 9) sequences of SHELgamma.

BEST METHOD OF PERFORMING THE INVENTION

10 The recombinant and synthetic procedures used for the synthesis of the derivatives, variants, expression products and hybrid molecules of the invention are described in standard texts such as Sambrook et al (1989).

15 Tropoelastin nucleotide sequences may be modified so as to provide derivatives, variants, expression products or hybrid molecules, by conventional site-directed or random mutagenesis. The sequences may also be modified by oligonucleotide-directed mutagenesis, which comprises the following steps:

- 20 1. synthesis of an oligonucleotide with a sequence that contains the desired nucleotide substitution (mutation);
2. hybridising the oligonucleotide to a template comprising a structural sequence encoding
25 tropoelastin; and
3. using a DNA polymerase to extend the oligonucleotide as a primer.

Another approach which is particularly suited to situations where a synthetic polynucleotide encoding the
30 tropoelastin derivative is prepared from oligonucleotide blocks bounded by restriction sites, is cassette mutagenesis where entire restriction fragments are replaced.

35 Purification of the derivatives, variants, expression products or hybrid molecules of the invention is performed using standard techniques including HPLC. The actual sequence of steps in the purification of a particular derivative, variant, expression product or hybrid molecule

is limited by the environment from which the molecule is to be purified. By way of example, reference is made to the purification scheme disclosed in WO94/14958.

Formulations in accordance with the invention are
5 formulated in accordance with standard techniques.

The amount of derivative, variant, expression product or hybrid molecule that may be combined with a carrier or diluent to produce a single dosage will vary depending on the situation in which the formulation is to be used and
10 the particular mode of administration.

It will be understood also that specific doses for any particular host may be influenced by factors such as the age, sex, weight and general health of the host as well as the particular characteristics of the derivative,
15 variant, expression product or hybrid molecule of the invention being used, and how it is administered.

Injectable preparations, for example, sterile injectable aqueous or oleagenous suspensions may be formulated according to the known art using suitable
20 dispersing or wetting agents and suspending agents. The sterile injectable preparation may also be a sterile injectable solution or suspension in a non-toxic parenterally acceptable diluent or solvent. Among the acceptable vehicles or solvents that may be employed are
25 water, Ringer's solution, alcohols and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono- or diglycerides. In addition,
30 fatty acids such as oleic acid and organic solvents find use in the preparation of injectables.

Routes of administration, dosages to be administered as well as frequency of administration are all factors which can be optimised using ordinary skill in the art.

35 In addition, the derivatives, variants, expression products and hybrid molecules of the invention may be prepared as topical preparations for instance as anti-wrinkle and hand lotions using standard techniques for the

preparation of such formulations. They may be prepared in aerosol form for, for instance, administration to a patient's lungs, or in the form of surgical implants, foods or industrial products by standard techniques.

5

SHEL

The preparation of SHEL is described in WO94/14958. It is directly expressed as a full length human protein with a calculated molecular weight of 64kDa. The full
10 nucleotide sequence and corresponding amino acid sequence of SHEL is shown in Figure 1. The preparation of pSHELF is described in WO94/14958.

pSHELF differs from the natural coding sequence(s) in a number of ways. As described in WO94/14958, the
15 untranslated regions present in the tropoelastin cDNA sequence were disregarded in designing the synthetic gene, and the nucleotides encoding the signal peptide were removed. Restriction endonuclease recognition sites were incorporated at regular intervals into the gene by
20 typically altering only the third base of the relevant codons, thereby maintaining the primary sequence of the gene product. The facility for silent alteration of the coding sequence was also exploited to change the codon bias of the tropoelastin gene to that commonly found in highly
25 expressed *E.coli* genes. [Genetics Computer Group (GCG) package version 7-UNIX using Codon Frequency and Gen Run Data: ecohigh-cod]. Two additional stop codons were added to the 3'-end, and an ATG start codon comprising a novel NcoI site was appended to the 5'-end. *Bam* HI cloning sites
30 were engineered at both ends of the synthetic sequence. Since the gene contains no internal methionine residues, treatment of the newly-synthesized gene product (expressed directly or as a fusion with another gene) with cyanogen bromide would liberate a protein with the same or similar
35 sequence as one form of natural tropoelastin comprising 731 amino acids. Other forms of processing are envisaged, which may generate tropoelastin species of the same or different lengths.

Two stop codons were added in order to allow the possible use of the construct in suppressor hosts, and also to avoid any potential depletion of termination (release) factors for translation.

5 As described in the following examples, the derivatives, pSHELF δ 26A, pSHELF δ modified, pSHELFgamma, pSHELF31-36, pSHELF32-36 and pSHELFgamma δ 26A were derived from the pSHELF nucleotide sequence. These particular derivatives, and indeed the derivatives, variants,
10 expression products and hybrid molecules of the invention can equally be derived from a native human or non-human tropoelastin nucleotide sequence.

Example 1: Construction of pSHELF δ 26A and pSHELF δ
15 modified

Mutagenesis was used with pSHELF to remove DNA corresponding to exon 26A. The sequence of the mutagenic primer was:

5'CGG GTT TCG GTG CTG TTC CGG GCG CGC TGG 3'

20 This flanked either side of exon 26A by 15bp resulting in its precise deletion. A second selection primer, which mutates a unique restriction site to another restriction site is normally used in the protocol but was not in this case since deletion of exon 26A also resulted
25 in the deletion of a unique restriction site, *Pml*I. The enzyme *Pml*I was used to treat the mutation reaction to linearise any unmutated parental plasmid and consequently to enrich for mutant plasmid. The reaction mixture was used to transform competent BMH17-18 *mutS E. coli*,
30 defective in mismatch repair, by electroporation and the entire transformed culture was grown overnight in LB+ampicillin. Mixed plasmid DNA, containing both mutated and parental plasmids, was isolated from the culture and the plasmid DNA was digested with *Pml*I to linearise the
35 parental plasmid. The plasmid DNA, now enriched for mutated plasmid, was used to transform *E. coli* HMS174 by electroporation and transformants selected on LB plates

containing $75\mu\text{gml}^{-1}$ ampicillin.

Colonies were grown overnight and plasmid mini-preparations performed. Constructs were screened using *PmlI* and those which were insensitive to digestion were further screened by *KpnI/PstI* double digestion. Candidate clones were sequenced to verify the sequence, named pSHELF δ modified.

Sequencing confirmed the region immediately surrounding the deletion was correct. *PstI* and *BssHII* restriction sites surrounding the correct region of pSHELF δ modified were used to remove the desired segment and re-insert it into the corresponding site of pSHELF. $6.5\mu\text{g}$ pSHELF and $7.5\mu\text{g}$ pSHELF δ modified were digested with *BssHII*, precipitated and digested with *PstI*. The appropriate three fragments were gel-purified and ligated. DNA was transformed into *E. coli* XL1-Blue and transformants selected on plates containing $75\mu\text{gml}^{-1}$ ampicillin.

Plasmids were isolated by mini-preparations and screened using *BglI* digestion. A candidate clone was further analysed by restriction enzyme digestion and sequenced, and named pSHELF δ 26A.

Example 2: Synthesis of Exon 26A

The region of SHEL corresponding to exon 26A was amplified by PCR, with primers modified to introduce an in-frame *BamHI* site upstream and a stop codon downstream at the 3' end. Two forms were generated: one terminating in valine (26AV) and the other terminating in phenylalanine (26AF). These forms are as follows:

GADEGVRRSLSPELREGDPSSSQHLPSTPSSPRV with properties:

Molecular weight = 3588.80

Residues = 34

Average Residue Weight = 105.553

Charge = -1

Isoelectric point = 5.71

and

GADEGVRRSLSPELREGDPSSSQHLPSTPSSPRF

A 26A coding region was expressed as a glutathione S-transferase (GST) fusion protein.

5

Example 3: Glycosaminoglycan binding activity of Exon 26A

Ultrafiltration assay methodology was developed to examine and quantify interactions occurring *in vitro* between the 26A region and purified extracellular matrix glcosaminoglycans. GST26A fusion protein and tropoelastin were compared with GST and tropoelastin lacking exon 26A at physiologically relevant conditions of pH and ionic strength.

15 Experimental evidence supports the notion that peptide 26A (26AF and 26AV) binds GAGs. Immobilised heparin column binding shows that GST26A binds more tightly than does GST, and requires a higher sodium chloride concentration for elution (Figure 6B).
20 Furthermore, GST26A fusion protein binds radioactive heparin with greater efficiencies than GST, and these can be compared with GAGs including chondroitin sulphates and keratin sulphates. An implication of this is that GAGs binding to tropoelastin can be adjusted based upon the
25 content of 26A. Cross-linked tropoelastin would be expected to show differential binding to GAGs based on the relative amounts of SHEL vs. SHEL δ 26A.

In summary, these studies reveal that the 26A region is a functional glycosaminoglycan binding domain, which
30 functions in intact tropoelastin. It is also active when isolated as a fusion entity yet displays no detectable structure in the absence of bound GAG. Furthermore, panel competition studies indicate a preference for those GAGs found in close association with the elastic fibre in the
35 extracellular matrix.

Example 4: Construction of pSHELgamma, pSHEL31-36, pSHEL32-36 and pSHELgammaδ26A

pSHELgamma is derived from the pSHELgamma construct disclosed in WO94/14958. pSHEL31-36, pSHEL32-36 and
5 pSHELgammaδ26A were derived from pSHELgamma. pSHELgamma was modified by introducing an oligonucleotide linker at the KpnI site. This encoded a factor Xa cleavage site which could be utilised in subsequent constructs. PCR and
10 site directed mutagenesis was then used to generate further, shorter forms which provided fusions with GST. Constructs were DNA sequenced for verification. Induced protein was isolated as GST-fusion proteins, which were subsequently bound to glutathione agarose. Protease
15 cleavage was optional where fusion proteins were desired; otherwise the cleaved proteins and peptides were further purified by reverse phase HPLC.

INDUSTRIAL APPLICATION

The derivatives and expression products of the
20 invention are of use in *inter alia* the medical, pharmaceutical, veterinary and cosmetic fields.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WEISS, ANTHONY S
UNIVERSITY, SYDNEY
- (ii) TITLE OF INVENTION: TROPOELASTIN DERIVATIVES
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
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 - (C) CITY: NORTH SYDNEY
 - (D) STATE: NEW SOUTH WALES
 - (E) COUNTRY: AUSTRALIA
 - (F) ZIP: 2060
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU P08117
 - (B) FILING DATE: 18-JUL-1997
- (viii) ATTORNEY/AGENT INFORMATION:
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 - (C) TELEX: 26547

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCCATGGG TGGCGTTCCG GGTGCTATCC CGGGTGGCGT TCCGGGTGGT GTATTCTACC	60
CAGGCGCGGG TCTGGGTGCA CTGGGCGGTG GTGCGCTGGG CCCGGGTGGT AAACCGCTGA	120
AACCGGTTCC AGGCGGTCTG GCAGGTGCTG GTCTGGGTGC AGGTCTGGGC GCGTTCCCCG	180
CGGTTACCTT CCCGGGTGCT CTGGTTCCGG GTGGCGTTGC AGACGCAGCT GCTGCGTACA	240
AAGCGGCAAA GGCAGGTGCG GGTCTGGGCG GGGTACCAGG TGTGGCGGT CTGGGTGTAT	300
CTGCTGGCGC AGTTGTTCCG CAGCCGGGTG CAGGTGTAAA ACCGGGCAAA GTTCCAGGTG	360
TTGGTCTGCC GGGCGTATAC CCGGTGGTG TTCTGCCGGG CGCGCGTTTC CCAGGTGTTG	420
GTGTACTGCC GGGCGTTCCG ACCGGTGCAG GTGTTAAACC GAAGGCACCA GGTGTAGGCG	480
GCGCGTTTCG GGTATCCCG GGTGTTGGCC CGTTCGGTGG TCCGCAGCCA GCGTTCCGC	540
TGGGTTACCC GATCAAAGCG CCGAAGCTTC CAGGTGGCTA CGGTCTGCCG TACACCACCG	600
GTAAACTGCC GTACGGCTAC GGTCCGGGTG GCGTAGCAGG TGCTGCGGGT AAAGCAGGCT	660
ACCCAACCGG TACTGGTGTT GGTCCGCAGG CTGCTGCGGC AGCTGCGGCG AAGGCAGCAG	720
CAAAATTCGG CGCGGGTGCA GCGGGTGTTT TGCCGGGCGT AGGTGGTGCT GCGTTCCGG	780
GTGTTCCAGG TGCGATCCCG GGCATCGGTG GTATCGCAGG CGTAGGTACT CCGGCGGCCG	840

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CTGCGGCTGC	GGCAGCTGCG	GCGAAAGCAG	CTAAATACGG	TGCGGCAGCA	GGCCTGGTTC	900
CGGGTGGTCC	AGGCTTCGGT	CCGGGTGTTG	TAGGCGTTCC	GGGTGCTGGT	GTTCCGGGCG	960
TAGGTGTTCC	AGGTGCGGGC	ATCCCGGTTG	TACCGGGTGC	AGGTATCCCG	GGCGCTGCGG	1020
TTCCAGGTGT	TGTATCCCCG	GAAGCGGCAG	CTAAGGCTGC	TGCGAAAGCT	GCGAAATACG	1080
GAGCTCGTCC	GGGCGTTGGT	GTTGGTGGCA	TCCCGACCTA	CGGTGTAGGT	GCAGGCGGTT	1140
TCCCAGGTTT	CGGCGTTGGT	GTTGGTGGCA	TCCCGGGTGT	AGCTGGTGTT	CCGTCTGTTG	1200
GTGGCGTACC	GGGTGTTGGT	GGCGTTCCAG	GTGTAGGTAT	CTCCCCGGA	GCGCAGGCAG	1260
CTGCGGCAGC	TAAAGCAGCG	AAGTACGGCG	TTGGTACTCC	GGCGGCAGCA	GCTGCTAAAG	1320
CAGCGGCTAA	AGCAGCGCAG	TTCGGACTAG	TTCCGGGCGT	AGGTGTTGCG	CCAGGTGTTG	1380
GCGTAGCACC	GGGTGTTGGT	GTTGCTCCGG	GCGTAGGTCT	GGCACCGGGT	GTTGGCGTTG	1440
CACCAGGTGT	AGGTGTTGCG	CCGGGCGTTG	GTGTAGCACC	GGGTATCGGT	CCGGGTGGCG	1500
TTGCGGCTGC	TGCGAAATCT	GCTGCGAAGG	TTGCTGCGAA	AGCGCAGCTG	CGTGCAGCAG	1560
CTGGTCTGGG	TGCGGGCATC	CCAGGTCTGG	GTGTAGGTGT	TGGTGTTCCG	GGCCTGGGTG	1620
TAGGTGCAGG	GGTACCGGGC	CTGGGTGTTG	GTGCAGGCGT	TCCGGGTTTC	GGTGCTGGCG	1680
CGGACGAAGG	TGTACGTCGT	TCCCTGTCTC	CAGAACTGCG	TGAAGGTGAC	CCGTCCTCTT	1740
CCCAGCACCT	GCCGTCTACC	CCGTCCTCTC	CACGTGTTCC	GGGCGCGCTG	GCTGCTGCGA	1800
AAGCGGCGAA	ATACGGTGCA	GCGGTTCCGG	GTGTACTGGG	CGGTCTGGGT	GCTCTGGGCG	1860
GTGTTGGTAT	CCCGGGCGGT	GTTGTAGGTG	CAGGCCCAGC	TGCAGCTGCT	GCTGCGGCAA	1920
AGGCAGCGGC	GAAAGCAGCT	CAGTTCGGTC	TGGTTGGTGC	AGCAGGTCTG	GGCGGTCTGG	1980
GTGTTGGCGG	TCTGGGTGTA	CCGGGCGTTG	GTGGTCTGGG	TGGCATCCCG	CCGGCGGCGG	2040
CAGCTAAAGC	GGCTAAATAC	GGTGCAGCAG	GTCTGGGTGG	CGTTCTGGGT	GGTGCTGGTC	2100
AGTTCCCACT	GGGCGGTGTA	GCGGCACGTC	CGGGTTTCGG	TCTGTCCCCG	ATCTTCCCAG	2160
GCGGTGCATG	CCTGGGTAAA	GCTTGCGGCC	GTAAACGTAA	ATAATGATAG		2210

(A) LENGTH: 733 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser	Met	Gly	Gly	Val	Pro	Gly	Ala	Ile	Pro	Gly	Gly	Val	Pro	Gly	Gly
1				5					10					15	
Val	Phe	Tyr	Pro	Gly	Ala	Gly	Leu	Gly	Ala	Leu	Gly	Gly	Gly	Ala	Leu
			20					25					30		
Gly	Pro	Gly	Gly	Lys	Pro	Leu	Lys	Pro	Val	Pro	Gly	Gly	Leu	Ala	Gly
		35					40					45			
Ala	Gly	Leu	Gly	Ala	Gly	Leu	Gly	Ala	Phe	Pro	Ala	Val	Thr	Phe	Pro
	50					55					60				
Gly	Ala	Leu	Val	Pro	Gly	Gly	Val	Ala	Asp	Ala	Ala	Ala	Ala	Tyr	Lys
65					70					75					80
Ala	Ala	Lys	Ala	Gly	Ala	Gly	Leu	Gly	Gly	Val	Pro	Gly	Val	Gly	Gly
				85					90					95	
Leu	Gly	Val	Ser	Ala	Gly	Ala	Val	Val	Pro	Gln	Pro	Gly	Ala	Gly	Val
			100						105				110		
Lys	Pro	Gly	Lys	Val	Pro	Gly	Val	Gly	Leu	Pro	Gly	Val	Tyr	Pro	Gly
		115					120					125			
Gly	Val	Leu	Pro	Gly	Ala	Arg	Phe	Pro	Gly	Val	Gly	Val	Leu	Pro	Gly
	130					135					140				
Val	Pro	Thr	Gly	Ala	Gly	Val	Lys	Pro	Lys	Ala	Pro	Gly	Val	Gly	Gly
145					150					155					160
Ala	Phe	Ala	Gly	Ile	Pro	Gly	Val	Gly	Pro	Phe	Gly	Gly	Pro	Gln	Pro

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	165		170		175
Gly Val Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly					
	180		185		190
Tyr Gly Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro					
	195		200		205
Gly Gly Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr					
	210		215		220
Gly Val Gly Pro Gln Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala					
	225		230		235 240
Lys Phe Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala					
		245		250	255
Gly Val Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala					
	260		265		270
Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys					
	275		280		285
Ala Ala Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly					
	290		295		300
Phe Gly Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val					
	305		310		315 320
Gly Val Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro					
		325		330	335
Gly Ala Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala					
	340		345		350
Ala Ala Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly					
	355		360		365
Gly Ile Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly					
	370		375		380
Val Gly Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Ser Val Gly					
	385		390		395 400
Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu					
	405		410		415

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Ala Gln Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Val Gly Thr
420 425 430

Pro Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly
435 440 445

Leu Val Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly
450 455 460

Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala
465 470 475 480

Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly
485 490 495

Pro Gly Gly Val Ala Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala
500 505 510

Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly
515 520 525

Leu Gly Val Gly Val Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val
530 535 540

Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala
545 550 555 560

Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp
565 570 575

Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val
580 585 590

Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val
595 600 605

Pro Gly Val Leu Gly Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro
610 615 620

Gly Gly Val Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Lys
625 630 635 640

Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu
645 650 655

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Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu
 660 665 670

Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala
 675 680 685

Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly
 690 695 700

Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly
 705 710 715 720

Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
 725 730

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
 1 5 10 15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
 20 25 30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
 35 40 45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
 50 55 60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Tyr Lys Ala Ala
 65 70 75 80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly

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	85		90		95
Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro					
	100		105		110
Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val					
	115		120		125
Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro					
	130		135		140
Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe					
	145		150		155
					160
Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val					
		165		170	
					175
Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly					
		180		185	
					190
Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly					
	195		200		205
Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val					
	210		215		220
Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe					
	225		230		235
					240
Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val					
		245		250	
					255
Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val					
		260		265	
					270
Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala					
	275		280		285
Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly					
	290		295		300
Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val					
	305		310		315
					320
Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala					
		325		330	
					335

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Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
340 345 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
355 360 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
370 375 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Ser Val Gly Gly Val
385 390 395 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
405 410 415

Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Val Gly Thr Pro Ala
420 425 430

Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val
435 440 445

Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly
450 455 460

Val Ala Pro Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly
465 470 475 480

Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly
485 490 495

Gly Val Ala Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala
500 505 510

Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly
515 520 525

Val Gly Val Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly
530 535 540

Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly Ala Val Pro Gly Ala
545 550 555 560

Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val
565 570 575

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Leu Gly Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val
 580 585 590

Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala
 595 600 605

Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu
 610 615 620

Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile
 625 630 635 640

Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu
 645 650 655

Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala
 660 665 670

Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys
 675 680 685

Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
 690 695

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1983 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGGGTGGCG TTCCGGGTGC TGTTCGGGGT GGC GTTCCGG GTGGTGTATT CTACCCAGGC 60

GCGGGTTTCG GTGCTGTTCC GGGTGGCGTT GCAGACGCAG CTGCTGCGTA CAAAGCGGCA 120

AAGGCAGGTG CGGGTCTGGG CGGGGTACCA GGTGTTGGCG GTCTGGGTGT ATCTGCTGGC 180
GCAGTTGTTC CGCAGCCGGG TGCAGGTGTA AAACCGGGCA AAGTTCAGG TGTGGTCTG 240
CCGGGCGTAT ACCCGGGTTT CGGTGCTGTT CCGGGCGCGC GTTTCACAGG TGTGGTGTGTA 300
CTGCCGGGCG TTCCGACCGG TGCAGGTGTT AAACCGAAGG CACCAGGTGT AGGCGGCGCG 360
TTCGCGGGTA TCCCGGGTGT TGGCCCGTTC GGTGGTCCGC AGCCAGGCGT TCCGCTGGGT 420
TACCCGATCA AAGCGCCGAA GCTTCCAGGT GGCTACGGTC TGCCGTACAC CACCGGTAAA 480
CTGCCGTACG GCTACGGTCC GGGTGGCGTA GCAGGTGCTG CGGGTAAAGC AGGCTACCCA 540
ACCGGTACTG GTGTTGGTCC GCAGGCTGCT GCGGCAGCTG CGGCGAAGGC AGCAGCAAAA 600
TTCGGCGCGG GTGCAGCGGG TTTCGGTGCT GTTCCGGGCG TAGGTGGTGC TGGCGTCCG 660
GGTGTTCAG GTGCGATCCC GGGCATCGGT GGTATCGCAG GCGTAGGTAC TCCGGCGGCC 720
GCTGCGGCTG CGGCAGCTGC GGCAGAAAGCA GCTAAATACG GTGCGGCAGC AGGCCGTGTT 780
CCGGGTGGTC CAGGCTTCGG TCCGGGTGTT GTAGGCGTTC CGGGTTCGG TGCTGTTCCG 840
GGCGTAGGTG TTCCAGGTGC GGGCATCCCC GTTGTACCGG GTGCAGGTAT CCCGGGCGCT 900
GCGGGTTTCG GTGCTGTATC CCCGGAAGCG GCAGCTAAGG CTGCTGCGAA AGCTGCGAAA 960
TACGGAGCTC GTCCGGGCGT TGGTGTGGT GGCATCCCGA CCTACGGTGT AGGTGCAGGC 1020
GGTTTCCCAG GTTTCGGCGT TGGTGTGGT GGCATCCCGG GTGTAGCTGG TGTTCCTCT 1080
GTTGGTGGCG TACCGGGTGT TGGTGGCGTT CCAGGTGTAG GTATCTCCCC GGAAGCGCAG 1140
GCAGCTGCGG CAGCTAAAGC AGCGAAGTAC GGCCTTGGTA CTCCGGCGGC AGCAGCTGCT 1200
AAAGCAGCGG CTAAAGCAGC GCAGTTCGGA CTAGTTCCGG GCGTAGGTGT TGCGCCAGGT 1260
GTTGGCGTAG CACCGGGTGT TGGTGTGCT CCGGGCGTAG GTCTGGCACC GGGTGTGGC 1320
GTTGCACCAG GTGTAGGTGT TGCGCCGGG GTTGGTGTAG CACCGGGTAT CGGTCCGGGT 1380
GGCGTTGCGG CTGCTGCGAA ATCTGCTGCG AAGGTTGCTG CGAAAGCGCA GCTGCGTGCA 1440
GCAGCTGGTC TGGGTGCGG CATCCCAGGT CTGGGTGTAG GTGTTGGTGT TCCGGGCTG 1500

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GGTGTAGGTG CAGGGGTACC GGGCCTGGGT GTTGGTGCAG GCGTTCCGGG TTTCGGTGCT      1560
GTTCCGGGCG CGCTGGCTGC TGC GAAAGCG GCGAAATACG GTGCTGTTCG GGGTGTACTG      1620
GGCGGTCTGG GTGCTCTGGG CGGTGTTGGT ATCCCGGGCG GTGTTGTAGG TGCAGGCCCA      1680
GCTGCAGCTG CTGCTGCGGC AAAGGCAGCG GCGAAAGCAG CTCAGTTCGG TCTGGTTGGT      1740
GCAGCAGGTC TGGGCGGTCT GGGTGTGGC GGTCTGGGTG TACCGGGCGT TGGTGGTCTG      1800
GGTGGCATCC CGCCGGCGGC GGCAGCTAAA GCGGCTAAAT ACGGTGCAGC AGGTCTGGGT      1860
GGCGTTCTGG GTGGTGCTGG TCAGTTCCCA CTGGGCGGTG TAGCGGCACG TCCGGGTTTC      1920
GGTCTGTCCC CGATCTTCCC AGGCGGTGCA TGCCTGGGTA AAGCTTGCGG CCGTAAACGT      1980
AAA                                                                    1983

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Gly Gly Val Pro Gly Ala Val Pro Gly Gly Val Pro Gly Gly Val
1           5           10           15
Phe Tyr Pro Gly Ala Gly Phe Gly Ala Val Pro Gly Gly Val Ala Asp
          20           25           30
Ala Ala Ala Ala Tyr Lys Ala Ala Lys Ala Gly Ala Gly Leu Gly Gly
          35           40           45
Val Pro Gly Val Gly Gly Leu Gly Val Ser Ala Gly Ala Val Val Pro
          50           55           60

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Gln Pro Gly Ala Gly Val Lys Pro Gly Lys Val Pro Gly Val Gly Leu
 65 70 75 80

Pro Gly Val Tyr Pro Gly Phe Gly Ala Val Pro Gly Ala Arg Phe Pro
 85 90 95

Gly Val Gly Val Leu Pro Gly Val Pro Thr Gly Ala Gly Val Lys Pro
 100 105 110

Lys Ala Pro Gly Val Gly Gly Ala Phe Ala Gly Ile Pro Gly Val Gly
 115 120 125

Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu Gly Tyr Pro Ile Lys
 130 135 140

Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro Tyr Thr Thr Gly Lys
 145 150 155 160

Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Ala Ala Gly Lys Ala
 165 170 175

Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala Ala Ala Ala Ala
 180 185 190

Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly Ala Ala Gly Phe Gly
 195 200 205

Ala Val Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly Ala
 210 215 220

Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala Ala
 225 230 235 240

Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Ala
 245 250 255

Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val
 260 265 270

Pro Gly Phe Gly Ala Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile
 275 280 285

Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Gly Phe Gly Ala
 290 295 300

Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr

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305		310		315		320
Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val						
	325			330		335
Gly Ala Gly Phe Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro						
	340			345		350
Gly Val Ala Gly Val Pro Ser Val Gly Gly Val Pro Gly Val Gly Gly						
	355			360		365
Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Ala						
	370			375		380
Lys Ala Ala Lys Tyr Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys						
	385			390		395
						400
Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val						
	405			410		415
Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val						
	420			425		430
Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro						
	435			440		445
Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala						
	450			455		460
Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala						
	465			470		475
						480
Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val						
	485			490		495
Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala						
	500			505		510
Gly Val Pro Gly Phe Gly Ala Val Pro Gly Ala Leu Ala Ala Ala Lys						
	515			520		525
Ala Ala Lys Tyr Gly Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala						
	530			535		540
Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala						
	545			550		555
						560

Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly
565 570 575

Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly
580 585 590

Val	Pro	Gly	Val	Gly	Gly	Leu	Gly	Gly	Ile	Pro	Pro	Ala	Ala	Ala	Ala
		595					600					605			

Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly
610 615 620

Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly
625 630 635 640

Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly
645 650 655

Arg Lys Arg Lys
660

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCGCCATGG GAGGTGTTCC GGGCGCGCTG GCTGCTGCGA AAGCGGCGAA ATACGGTGCA 60

GCGGTTCCGG GTGTACTGGG CGGTCTGGGT GCTCTGGGCG GTGTTGGTAT CCCGGGCGGT 120

GTTGTAGGTG CAGGCCAGC TGCAGCTGCT GCTGCGGCAA AGGCAGCGGC GAAAGCAGCT 180

CAGTTCGGTC TGGTTGGTGC AGCAGGTGTG GGCGGTCTGG GTGTTGGCGG TCTGGGTGTA 240
 CCGGGCGTTG GTGGTCTGGG TGGCATCCCG CCGGCGGCGG CAGCTAAAGC GGCTAAATAC 300
 GGTGCAGCAG GTCTGGGTGG CGTTCTGGGT GGTGCTGGTC AGTTCCCACT GGGCGGTGTA 360
 GCGGCACGTC CGGGTTTCGG TCTGTCCCCG ATCTTCCCAG GCGGTGCATG CCTGGGTAAA 420
 GCTTGCGGCC GTAAACGTAA A 441

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Ala Met Gly Gly Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala
 1 5 10 15
 Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu
 20 25 30
 Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala
 35 40 45
 Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu
 50 55 60
 Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val
 65 70 75 80
 Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys
 85 90 95
 Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala
 100 105 110

Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu
115 120 125

Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg
130 135 140

Lys Arg Lys
145

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCCGCCATGG GAGCTCTGGT AGGCCTGGGC GTACCGGGCC TGGGTGTTGG TGCAGGCGTT	60
CCGGGTTTCG GTGCTGGCGC GGACGAAGGT GTACGTCGTT CCCTGTCTCC AGAACTGCGT	120
GAAGGTGACC CGTCCTCTTC CCAGCACCTG CCGTCTACCC CGTCCTCTCC ACGTGTTCCG	180
GGCGCGCTGG CTGCTGCGAA AGCGGCGAAA TACGGTGCAG CGGTTCCGGG TGTACTGGGC	240
GGTCTGGGTG CTCTGGGCGG TGTGGGTATC CCGGGCGGTG TTGTAGGTGC AGGCCAGCT	300
GCAGCTGCTG CTGCGGCAAA GGCAGCGGCG AAAGCAGCTC AGTTCGGTCT GGTGGTGCA	360
GCAGGTCTGG GCGGTCTGGG TGTGGCGGT CTGGGTGTAC CGGGCGTTGG TGGTCTGGGT	420
GGCATCCCGC CGGCGGCGGC AGCTAAAGCG GCTAAATACG GTGCAGCAGG TCTGGGTGGC	480
GTTCTGGGTG GTGCTGGTCA GTTCCCACTG GCGGTGTAG CGGCACGTCC GGGTTTCGGT	540

CTGTCCCCGA TCTTCCCAGG CGGTGCATGC CTGGGTAAAG CTTGCGGCCG TAAACGTAAA 600

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Ala Met Gly Ala Leu Val Gly Leu Gly Val Pro Gly Leu Gly Val
1 5 10 15

Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg
20 25 30

Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln
35 40 45

His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala
50 55 60

Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly
65 70 75 80

Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly
85 90 95

Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala
100 105 110

Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val
115 120 125

Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro
130 135 140

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Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly
 145 150 155 160

Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg
 165 170 175

Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly
 180 185 190

Lys Ala Cys Gly Arg Lys Arg Lys
 195 200

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Ile Pro Pro Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala
 1 5 10 15

Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly
 20 25 30

Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly
 35 40 45

Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
 50 55 60

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro
1 5 10 15

Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe
 20 25 30

Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu Leu Arg Glu
1 5 10 15

Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro Ser Ser Pro
 20 25 30

Arg Val

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu Leu Arg Glu
1 5 10 15

Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro Ser Ser Pro
 20 25 30

Arg Phe

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val
1 5 10 15

Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val
 20 25 30

Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg
 35 40 45

Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln
 50 55 60

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His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala
 65 70 75 80

Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly
 85 90 95

Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly
 100 105 110

Ala Gly Pro Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala
 115 120 125

Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val
 130 135 140

Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro
 145 150 155 160

Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly
 165 170 175

Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg
 180 185 190

Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly
 195 200 205

Lys Ala Cys Gly Arg Lys Arg Lys
 210 215

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val

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1	5	10	15
Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val			
20	25	30	
Gly Ala Gly Val Pro Gly Phe Gly Ala Val Pro Gly Ala Leu Ala Ala			
35	40	45	
Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly			
50	55	60	
Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala			
65	70	75	80
Gly Pro Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala			
85	90	95	
Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly			
100	105	110	
Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala			
115	120	125	
Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val			
130	135	140	
Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro			
145	150	155	160
Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys			
165	170	175	
Ala Cys Gly Arg Lys Arg Lys			
180			

THE CLAIMS:

1. A human tropoelastin derivative or an amino acid
sequence variant thereof, wherein the derivative or
5 variant has elastin-like properties.

2. A human tropoelastin derivative or an amino acid
sequence variant thereof, wherein the derivative or
variant has macro-molecular binding properties.

10

3. A derivative or variant thereof according to
claim 2 wherein the macro-molecular binding properties
include the ability to bind glycosyaminoglycans.

15

4. A human tropoelastin derivative or an amino acid
sequence variant thereof, wherein the derivative or
variant has elastin-like properties and macro-molecular
binding properties.

20

5. A polynucleotide encoding a derivative or
variant thereof of any one of claims 1 to 4.

6. A tropoelastin derivative comprising the amino
acid sequence of SHEL δ modified, or an amino acid sequence
25 variant of the derivative comprising the amino acid
sequence of SHEL δ modified.

7. A tropoelastin derivative according to claim 6
comprising SEQ ID NO: 5.

30

8. A polynucleotide encoding a tropoelastin
derivative, the derivative comprising the amino acid
sequence of SHEL δ modified or an amino acid sequence
variant of the derivative comprising the amino acid
35 sequence of SHEL δ modified.

9. A polynucleotide according to claim 8 comprising
SEQ ID NO: 4.

10. A synthetic polynucleotide encoding a
5 tropoelastin derivative, the derivative comprising the
amino acid sequence of SHELδ26A or an amino acid sequence
variant of the derivative comprising the amino acid
sequence of SHELδ26A.

10 11. A synthetic polynucleotide according to claim
10, the polynucleotide comprising the sequence of from
nucleotide position 1 to 1676 contiguous with the sequence
of from nucleotide position 1775 to 2210 of SEQ ID NO: 1.

15 12. An amino acid sequence variant of the derivative
comprising the amino acid sequence of SHELδ26A.

13. An amino acid sequence variant according to
claim 12 comprising SEQ ID NO:3.

20

14. A tropoelastin derivative comprising the amino
acid sequence of SHELgamma, or an amino acid sequence
variant of the derivative comprising the amino acid
sequence of SHELgamma.

25

15. A tropoelastin derivative according to claim 14
comprising SEQ ID NO:9.

16. A polynucleotide encoding a tropoelastin
30 derivative, the derivative comprising the amino acid
sequence of the derivative SHELgamma, or an amino acid
sequence variant of the derivative comprising the amino
acid sequence of SHELgamma.

35 17. A polynucleotide sequence according to claim 16
comprising SEQ ID NO:8.

18. A tropoelastin derivative comprising the amino acid sequence of SHELgamma excluding exon 26A, or an amino acid sequence variant of the derivative comprising the amino acid sequence of SHELgamma excluding exon 26A.

5

19. A tropoelastin derivative according to claim 18 comprising SEQ ID NO:7.

20. A polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHELgamma excluding exon 26A or an amino acid sequence variant of the derivative comprising the amino acid sequence of SHELgamma excluding exon 26A.

21. A polynucleotide sequence according to claim 20 comprising SEQ ID NO: 6.

22. A tropoelastin derivative comprising the amino acid sequence of SHEL31-36, or an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL31-36.

23. A tropoelastin derivative according to claim 22 comprising SEQ ID NO: 10.

25

24. A polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHEL31-36 or an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL31-36.

30

25. A polynucleotide according to claim 24, the polynucleotide comprising the sequence of from nucleotide position 2022 to 2210 of SEQ ID NO: 1.

35

26. A tropoelastin derivative comprising the amino acid sequence of SHEL32-36, or an amino acid sequence variant of the derivative comprising the amino acid

sequence of SHEL32-36.

27. A tropoelastin derivative according to claim 26 comprising SEQ ID NO: 11.

5

28. A polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHEL32-36 or an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL32-36.

10

29. A polynucleotide according to claim 28, the polynucleotide comprising the sequence of from nucleotide position 2061 to 2210 of SEQ ID NO: 1.

15

30. A tropoelastin derivative comprising the amino acid sequence of peptide 26A, or an amino acid sequence variant of the derivative comprising the amino acid sequence of peptide 26A.

20

31. A tropoelastin derivative according to claim 30 comprising SEQ ID NO: 12 or SEQ ID NO: 13.

32. A polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of peptide 26A or an amino acid sequence variant of the derivative comprising the amino acid sequence of peptide 26A.

25

33. A polynucleotide according to claim 32, the polynucleotide comprising the sequence of from nucleotide position 1677 to 1774 of SEQ ID NO: 1.

30

34. A tropoelastin derivative comprising the amino acid sequence of SHEL26-36, or an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL26-26.

35

35. A tropoelastin derivative according to claim 34 comprising SEQ ID NO: 14.

5 36. A polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHEL26-36 or an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL26-36.

10 37. A polynucleotide according to claim 36, the polynucleotide comprising the sequence of from nucleotide position 1554 to 2210 of SEQ ID NO: 1.

15 38. A tropoelastin derivative comprising the amino acid sequence of SHEL26-26 excluding exon 26A, or an amino acid sequence variant of the derivative comprising the amino acid sequence of SHEL26-26 excluding exon 26A.

20 39. A tropoelastin derivative according to claim 38 comprising SEQ ID NO: 15.

25 40. A polynucleotide encoding a tropoelastin derivative, the derivative comprising the amino acid sequence of SHEL26-26 excluding exon 26A or an amino acid sequence variant of the derivative of SHEL26-26 excluding exon 26A.

30 41. A polynucleotide according to claim 40, the polynucleotide comprising the sequence of from nucleotide position 1554 to 1676 contiguous with the sequence of from nucleotide position 1776 to 2210 of SEQ ID NO: 1.

35 42. A vector comprising a polynucleotide according to any one of claims 5, 8, 9, 16, 17, 20, 21, 24, 25, 28, 29, 32, 33, 36, 37, 40 or 41, or a synthetic polynucleotide according to claim 10 or 11.

43. The vector according to claim 42 wherein the

polynucleotide or synthetic polynucleotide is operatively linked to a promoter or enhancer regulatory sequence.

44. The vector according to claim 42 or 43 wherein
5 the polynucleotide or synthetic polynucleotide is operatively linked to a nucleotide sequence, the nucleotide sequence encoding a further amino acid sequence.

10 45. A cell containing a vector according to any one of claims 42 to 44.

46. A method for producing a derivative of tropoelastin or an amino acid sequence variant of the
15 derivative, the method comprising:

- (a) providing a vector according to any one of claims 42 to 44;
- (b) introducing the vector into a cell;
- (c) maintaining the cell in conditions suitable
20 for expression of the vector; and
- (d) isolating the tropoelastin derivative or variant.

47. A tropoelastin derivative or variant produced by
25 the method of claim 46.

48. A transgenic non-human animal containing a vector according to any one of claims 42 to 44, or a polynucleotide according to any one of claims 5, 8, 9, 16,
30 17, 20, 21, 24, 25, 28, 29, 32, 33, 36, 37, 40 or 41, or a synthetic polynucleotide according to claim 10 or 11.

49. A tropoelastin derivative or variant of the derivative produced by a transgenic animal according to
35 claim 48

50. method for producing a tropoelastin derivative or a variant of the derivative according to any one of

claims 1-4, 6, 7, 12-15, 18, 19, 22, 23, 26, 27, 30, 31, 34, 35, 38 or 39, the method comprising producing the tropoelastin derivative or variant by solid-phase peptide synthesis.

5

51. A tropoelastin derivative or variant produced by the method of claim 50.

52. A formulation comprising at least one tropoelastin derivative or variant of the derivative according to any one of 1-4, 6, 7, 12-15, 18, 19, 22, 23, 26, 27, 30, 31, 34, 35, 38, 39, 47 or 49, together with a pharmaceutically acceptable carrier or diluent.

53. An expression product comprising a tropoelastin derivative or variant of the derivative according to any one of claims 1-4, 6, 7, 12-15, 18, 19, 22, 23, 26, 27, 30, 31, 34, 35, 38, 39, 47 or 49, and a further amino acid sequence.

20

54. An expression product according to claim 53 wherein the tropoelastin derivative comprises the amino acid sequence of peptide 26A, or an amino acid sequence variant of the derivative comprising the amino acid sequence of peptide 26A.

25

55. A polynucleotide encoding an expression product according to claims 53 or 54.

56. A vector comprising the polynucleotide according to claim 55.

30

57. A cell containing a vector according to claim 56.

35

58. A method for producing an expression product according to claim 52 or 54, the method comprising:

(a) providing a vector according to claim 56;

- (b) introducing the vector into a cell;
- (c) maintaining the cell in conditions suitable for expression of the vector; and
- (d) isolating the expression product.

5

59. An expression product produced by the method of claim 58.

10

60. An transgenic non-human animal containing a vector according to claim 56 or a polynucleotide according to claim 55.

15

61. An expression product produced by a transgenic animal according to claim 60.

20

62. A formulation comprising at least one expression product according to any of claims 53, 54, 59 or 61, together with a pharmaceutically acceptable carrier or diluent.

25

63. A hybrid molecule comprising a biological polymer wherein the polymer is linked to a tropoelastin derivative comprising the amino acid sequence of peptide 26A or an amino acid sequence variant of the derivative comprising peptide 26A.

64. A hybrid molecule according to claim 63 wherein the biological polymer is a protein.

30

65. A hybrid molecule according to claim 64 wherein in the protein is selected from the group consisting of cytokines, growth factors and antibodies.

35

66. A hybrid molecule according to claim 63 wherein the biological polymer is selected from the group consisting of lipids, sugars and nucleic acids.

67. A polynucleotide sequence encoding a hybrid molecule according to claim 64.

68. A vector comprising a polynucleotide sequence according to claim 67.

5 69. A cell containing a vector according to claim 68.

70. A method for producing a hybrid molecule according to claim 64, the method comprising:

- 10 (a) providing a vector according to claim 68;
 (b) introducing the vector into a cell;
 (c) maintaining the cell in conditions suitable for expression of the vector; and
 (d) isolating the hybrid molecule.

15

71. A hybrid molecule produced by the method of claim 70.

20 72. A transgenic non-human animal containing a vector according to claim 68 or a polynucleotide according to claim 67.

73. A hybrid molecule produced by a transgenic animal according to claim 72.

25

74. A hybrid molecule comprising a synthetic polymer linked to peptide 26A or a variant of peptide 26A.

30 75. A formulation comprising at least one hybrid molecule according to any of claims 63-65, 71, 73 and 74, together with a pharmaceutically acceptable carrier or diluent.

76. A cross linked complex, the complex comprising at least one of the following:

- (i) at least one derivative or variant of the derivative according to any of 1-4, 6, 7, 12-15, 18, 19, 22, 23, 26, 27, 30, 31, 34, 35, 38, 39, 47

or 49;

(ii) at least expression product according to any of claims 53, 54, 58 or 61; and

5 (iii) at least one hybrid molecule according to any of claims 63-65, 71, 73 or 74.

77. An implant, the implant comprising at least one of the following:

10 (i) at least one derivative or variant of the derivative according to any of 1-4, 6, 7, 12-15, 18, 19, 22, 23, 26, 27, 30, 31, 34, 35, 38, 39, 47 or 49;

(ii) at least expression product according to any of claims 53, 54, 58 or 61; and

15 (iii) at least one hybrid molecule according to any of claims 63-65, 71, 73 or 74.

78. A method of imparting glycosaminoglycan binding activity to a biological polymer comprising the step of
20 linking a tropoelastin derivative comprising the amino acid sequence of peptide 26A, or an amino acid sequence variant of the derivative comprising the amino acid sequence of peptide 26A with the biological polymer.

25 79. A method of deleting glycosaminoglycan binding activity from a biological polymer comprising the step of deleting a tropoelastin derivative comprising the amino acid sequence of peptide 26A, or an amino acid sequence variant of the derivative comprising the amino acid
30 sequence of peptide 26A from the biological polymer.

80. The method of claim 66 or 67 wherein the biological polymer is a protein.

35 81. A formulation comprising a tropoelastin derivative or variant of the derivative and a synthetic or biological polymer.

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1 GATCCATGGGTGGCGTTCCGGGTGCTATCCCGGGTGGCGTTCCGGGTGGTGTATTCTACC 60
GTACCCACCGCAAGGCCACGATAGGGCCACCGCAAGGCCACACATAAGATGG
S M G G V P G A I P G G V P G G V F Y P

61 CAGGCGCGGGTCTGGGTGCACTGGGCGGTGGTGCCTGGGCCCCGGGTGGTAAACCGCTGA 120
GTCCGCGCCAGACCCACGTGACCGGCCACACGCGACCCGGGCCCCACCATTGCGGACT
G A G L G A L G G G A L G P G G K P L K

121 AACCGGTTCCAGGCGGTCTGGCAGGTGCTGGTCTGGGTGCAGGTCTGGGCGCGTTCCCGG 180
TTGGCCAAGGTCCGCCAGACCGTCCACGACCAGACCCACGTCCAGACCCGCGCAAGGGCC
P V P G G L A G A G L G A G L G A F P A

181 CGGTTACCTTCCCGGGTGCTCTGGTTCCGGGTGGCGTTGCAGACGCGAGCTGCTGCGTACA 240
GCCAATGGAAGGGCCCACGAGACCAAGGGCCACCGCAACGTCTGCGTCGACGACGCATGT
V T F P G A L V P G G V A D A A A A Y K

241 AAGCGGCAAAGGCAGGTGCGGGTCTGGGCGGGGTACCAGGTGTTGGCGGTCTGGGTGTAT 300
TTCGCCGTTTCCGTCCACGCCAGACCCGCCCCATGGTCCACAACCGCCAGACCCACATA
A A K A G A G L G G V P G V G G L G V S

301 CTGCTGGCGCAGTTGTTCCGCGGCCGGGTGCAGGTGTAAAACCGGGCAAGTTCCAGGTG 360
GACGACCGCGTCAACAAGGCGTCGGCCCCACGTCEACATTTTGGCCCGTTTCAAGGTCCAC
A G A V V P Q P G A G V K P G K V P G V

361 TTGGTCTGCCGGGCGTATACCCGGGTGGTGTCTGCCGGGCGCGCGTTTCCCAGGTGTTG 420
AACCAGACGGGCCCATATGGGCCCCACCAAGACGGCCCGCGCGCAAGGGTCCACAAC
G L P G V Y P G G V L P G A R F P G V G

Figure 1(1)

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421 GTGTACTGCCGGGCGTTCCGACCGGTGCAGGTGTTAAACCGAAGGCACCAGGTGTAGGCG 480
CACATGACGGCCCGCAAGGCTGGCCACGTCCACAATTTGGCTTCCGTGGTCCACATCCGC
V L P G V P T G A G V K P K A P G V G G

481 GCGCGTTCCGGGTATCCCGGGTGTGGCCCGTTCCGGTGGTCCGCAGCCAGGCGTTCCGC 540
CGCGCAAGCGCCCATAGGGCCCCACAACCGGGCAAGCCACCAGGCGTCGGTCCGCAAGGCG
A F A G I P G V G P F G G P Q P G V P L

541 TGGGTTACCCGATCAAAGCGCCGAAGCTTCCAGGTGGCTACGGTCTGCCGTACACCACCG 600
ACCCAATGGGCTAGTTTCGCGGCTTCGAAGGTCCACCGATGCCAGACGGCATGTGGTGGC
G Y P I K A P K L P G G Y G L P Y T T G

601 GTAACTGCCGTACGGCTACGGTCCGGGTGGCGTAGCAGGTGCTGCGGGTAAAGCAGGCT 660
CATTTGACGGCATGCCGATGCCAGGCCCACCGCATCGTCCACGACGCCCATTTTCGTCCGA
K L P Y G Y G P G G V A G A A G K A G Y

661 ACCCAACCGGTACTGGTGTGGTCCGCAGGCTGCTGCGGCAGCTGCGGGCGAAGGCAGCAG 720
TGGGTTGGCCATGACCACAACCAGGCGTCCGACGACGCCGTCGACGCGCGTTCCGTCGTC
P T G T G V G P Q A A A A A A A K A A A

721 CAAAATTCGGCGCGGGTGCAGCGGGTGTCTGCCGGGCGTAGGTGGTGTGCTGGCGTTCCGG 780
GTTTTAAGCCGCGCCACGTGCGCCACAAGACGGCCCCGCATCCACCACGACCGCAAGGCC
K F G A G A A G V L P G V G G A G V P G

781 GTGTTCCAGGTGCGATCCCGGGCATCGGTGGTATCGCAGGCGTAGGTACTCCGGCGGGCCG 840
CACAAGGTCCACGCTAGGGCCCCGTAGCCACCATAGCGTCCGCATCCATGAGGCCGCGCGC
V P G A I P G I G G I A G V G T P A A A

841 CTGCGGCTGCGGCAGCTGCGGCGAAGCAGCTAAATACGGTGCGGCAGCAGGCCTGGTTC 900
GACGCCGACGCGCTCGACGCGCGCTTTCGTGATTATGCCACGCGTCGTCCGGACCAAG
A A A A A A A K A A K Y G A A A G L V P

Figure 1(2)

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901 CGGGTGGTCCAGGCTTCGGTCCGGGTGTTGTAGGCGTTCCGGGTGCTGGTGTTCGGGGCG 960
GCCACACAGGTCCGAAGCCAGGCCCAACATCCGCAAGGCCACGACCACAAGGCCCGC
G G P G F G P G V V G V P G A G V P G V

961 TAGGTGTTCCAGGTGCGGGCATCCCGGTTGTACCGGGTGCAAGGTATCCCGGGCGCTGCGG 1020
ATCCACAAGGTCCACGCCCGTAGGGCCAACATGGCCCACGTCCATAGGGCCCGCGACGCC
G V P G A G I P V V P G A G I P G A A V

1021 TTCCAGGTGTTGTATCCCCGGAAGCGGCAGCTAAGGCTGCTGCGAAAGCTGCGAAATACG 1080
AAGGTCCACAACATAGGGGCCTTCGCCGTCGATTCCGACGACGCTTTCGACGCTTTATGC
P G V V S P E A A A K A A A K A A K Y G

1081 GAGCTCGTCCGGGCGTTGGTGTGGTGGCATCCCGACCTACGGTGTAGGTGCAGGCGGTT 1140
CTCGAGCAGGCCCGCAACCACAACCACCGTAGGGCTGGATGCCACATCCACGTCCGCCAA
A R P G V G V G G I P T Y G V G A G G F

1141 TCCCAGGTTTCGGGCGTTGGTGTGGTGGCATCCCGGGTGTAGCTGGTGTTCGCTCTGTTG 1200
AGGGTCCAAAGCCGCAACCACAACCACCGTAGGGCCACATCGACCACAAGGCAGACAAC
P G F G V G V G G I P G V A G V P S V G

1201 GTGGCGTACCGGGTGTGGTGGCGTTCCAGGTGTAGGTATCTCCCCGGAAGCGCAGGCAG 1260
CACCGCATGGCCCCACAACCACCGCAAGGTCCACATCCATAGAGGGGCCTTCGCGTCCGTC
G V P G V G G V P G V G I S P E A Q A A

1261 CTGCGGCAGCTAAAGCAGCGAAGTACGGCGTTGGTACTCCGGCGGCAGCAGCTGCTAAAG 1320
GACGCCGTCGATTTCGTCGCTTCATGCCGCAACCATGAGGCCGCCGTCGTCGACGATTTC
A A A K A A K Y G V G T P A A A A A K A

1321 CAGCGGCTAAAGCAGCGCAGTTCGGACTAGTTCGGGGCGTAGGTGTTGCGCCAGGTGTTG 1380
GTCGCCGATTTTCGTCGCGTCAAGCCTGATCAAGGCCCGCATCCACAACGGGTCCACAAC
A A K A A Q F G L V P G V G V A P G V G

Figure 1(3)

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1381 GCGTAGCACCGGGTGTGGTGTGGCTCCGGGCGTAGGTCTGGCACCAGGGTGTGGCGTTG 1440
CGCATCGTGGCCCAACCAACGAGGCCCGCATCCAGACCGTGGCCCAACCGCAAC
V A P G V G V A P G V G L A P G V G V A

1441 CACCAGGTGTAGGTGTGCGCCGGGCGTTGGTGTAGCACCGGGTATCGGTCCGGGTGGCG 1500
GTGGTCCACATCCACAACGCGGCCCGCAACCACATCGTGGCCCATAGCCAGGCCACCGC
P G V G V A P G V G V A P G I G P G G V

1501 TTGCGGCTGCTGCGAAATCTGCTGCGAAGGTTGCTGCGAAAGCGCAGCTGCGTGCAGCAG 1560
AACGCCGACGACGCTTTAGACGACGCTTCCAACGACGCTTTCGCGTCGACGCACGTCGTC
A A A A K S A A K V A A K A Q L R A A A

1561 CTGGTCTGGGTGCGGGCATCCCAGGTCTGGGTGTAGGTGTGGTGTTCGGGCCCTGGGTG 1620
GACCAGACCCACGCCCGTAGGGTCCAGACCCACATCCACAACCACAAGGCCCGGACCCAC
G L G A G I P G L G V G V G V P G L G V

1621 TAGGTGCAGGGGTACCGGGCCTGGGTGTGGTGCAGGCGTTCCGGGTTTCGGTGCTGGCG 1680
ATCCACGTCCCCATGGCCCGGACCCACAACCACGTCCGCAAGGCCCAAAGCCACGACCGC
G A G V P G L G V G A G V P G F G A G A

1681 CGGACGAAGGTGTACGTCGTTCCCTGTCTCCAGAAGTGCAGTGAAGGTGACCCGTCCTCTT 1740
GCCTGCTTCCACATGCAGCAAGGGACAGAGGTCTTGACGCACTTCCACTGGGCAGGAGAA
D E G V R R S L S P E L R E G D P S S S

1741 CCCAGCACCTGCCGTCTACCCCGTCTCTCCACGTGTTCCGGGCGCGCTGGCTGCTGCGA 1800
GGGTGCTGGACGGCAGATGGGGCAGGAGAGGTGCACAAGGCCCGCGCGACCGACGACGCT
Q H L P S T P S S P R V P G A L A A A K

1801 AAGCGGCGAAATACGGTGCAGCGGTTCCGGGTGTACTGGGCGGTCTGGGTGCTCTGGGCG 1860
TTCGCCGCTTTATGCCACGTGCGCAAGGCCACATGACCCGCCAGACCCACGAGACCCGC
A A K Y G A A V P G V L G G L G A L G G

Figure 1(4)

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1861 GTGTTGGTATCCCGGGCGGTGTTGTAGGTGCAGGCCAGCTGCAGCTGCTGCTGCGGCAA 1920
CACAACCATAGGGCCCGCCACAACATCCACGTCCGGGTCGACGTCGACGACGACGCCGTT
V G I P G G V V G A G P A A A A A A A K

1921 AGGCAGCGGCGAAAGCAGCTCAGTTCGGTCTGGTTGGTGCAGCAGGTCTGGGCGGTCTGG 1980
TCCGTCGCCGCTTTTCGTCGAGTCAAGCCAGACCAACCACGTCGTCAGACCCGCCAGACC
A A A K A A Q F G L V G A A G L G G L G

1981 GTGTTGGCGGTCTGGGTGTACCGGGCGTTGGTGGTCTGGGTGGCATCCCGCCGGCGGCGG 2040
CACAACCGCCAGACCCACATGGCCCGCAACCACCAGACCCACCGTAGGGCGGCCGCCGCC
V G G L G V P G V G G L G G I P P A A A

2041 CAGCTAAAGCGGCTAAATACGGTGCAGCAGGTCTGGGTGGCGTTCTGGGTGGTGCCTGGTC 2100
GTCGATTTGCGCGATTTATGCCACGTCGTCAGACCCACCGCAAGACCCACCACGACCAG
A K A A K Y G A A G L G G V L G G A G Q

2101 AGTTCCTCACTGGGCGGTGTAGCGGCACGTCCGGGTTTCGGTCTGTCCCGATCTTCCCAG 2160
TCAAGGGTGACCCGCCACATCGCCGTGCAGGCCCAAGCCAGACAGGGGCTAGAAGGGTC
F P L G G V A A R P G F G L S P I F P G

2161 GCGGTGCATGCCTGGGTAAAGCTTGCGGGCGTAAACGTAAATAATGATAG 2210
CGCCACGTACGGACCCATTTCGAACGCCGGCATTTCGATTTATTACTATCCTAG
G A C L G K A C G R K R K * * *

Figure 1(5)

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1  GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKFPVPGGLAGAGLG  50
1  GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKFPVPGGLAGAGLG  50
51  AGLGAFFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGLGVSAG  100
51  AGLGAFFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGLGVSAG  100
101  AVVPQPGAGVKPKVKPGVGLPGVYPGGVLPGARFPGVGVLPJVPTGAGVK  150
101  AVVPQPGAGVKPKVKPGVGLPGVYPGGVLPGARFPGVGVLPJVPTGAGVK  150
151  PKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKL  200
151  PKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKL  200
201  PYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAKAAKFGAGAAGVLPG  250
201  PYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAKAAKFGAGAAGVLPG  250
251  VGGAGVPGVPGAIPGIGGIAGVGTAAAAAAKAAKYGAAAGLVPGG  300
251  VGGAGVPGVPGAIPGIGGIAGVGTAAAAAAKAAKYGAAAGLVPGG  300
301  PGFGPGVVGVPAGVPGVGPAGIPVVPAGIPGAAPGVVSPAAAAKA  350
301  PGFGPGVVGVPAGVPGVGPAGIPVVPAGIPGAAPGVVSPAAAAKA  350
351  AAKAAKYGARPGVGVGGIPTTYGVGAGGFPGFVGVGGIPGVAGVPSVGGV  400
351  AAKAAKYGARPGVGVGGIPTTYGVGAGGFPGFVGVGGIPGVAGVPSVGGV  400
401  PGVGGVPGVGISPEAQAAAAKAAKYGVGTPAAAAKAAKAAQFGLVPG  450
401  PGVGGVPGVGISPEAQAAAAKAAKYGVGTPAAAAKAAKAAQFGLVPG  450
451  VGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAA  500
451  VGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAA  500
501  AAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGPGLGVGAGVPGLVGAG  550
501  AAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGPGLGVGAGVPGLVGAG  550
551  VPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAKAA  600
551  VPGFGA.....VPGALAAKAA  567
601  KYGAAVPGVIGGLGALGGVGIPGGVVGAGPAAAAAAKAAKAAQFGLVG  650
568  KYGAAVPGVIGGLGALGGVGIPGGVVGAGPAAAAAAKAAKAAQFGLVG  617
651  AAGLGGLVGGGLGVPGVGGGLGGIPAAAAKAAKYGAAGLGGVIGGAGQFP  700
618  AAGLGGLVGGGLGVPGVGGGLGGIPAAAAKAAKYGAAGLGGVIGGAGQFP  667
701  LGGVAARPFGFLSPIFFGGACLGKACGRKRK  731
668  LGGVAARPFGFLSPIFFGGACLGKACGRKRK  698

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Figure 2(1)

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1 ATGGGTGGCGTTCCGGGTGCTGTTCCGGGTGGCGTTCCGGGTGGTGTATT 50
1 MetGlyGlyValProGlyAlaValProGlyGlyValProGlyGlyValPh 17
51 CTACCCAGGCGCGGGTTTCGGTGTCTGTTCCGGGTGGCGTTTCAGACGCAG 100
18 eTyrProGlyAlaGlyPheGlyAlaValProGlyGlyValAlaAspAla 34
101 CTGCTGCGTACAAAGCGGCAAGGCAGGTGCGGGTCTGGGCGGGGTACCA 150
35 laAlaAlaTyrTysAlaAlaLysAlaGlyAlaGlyLeuGlyGlyValPro 50
151 GGTGTTGGCGGTCTGGGTGTATCTGCTGGCGCAGTTGTTCCGCAGCCGGG 200
51 GlyValGlyGlyLeuGlyValSerAlaGlyAlaValValProGlnProG 67
201 TGCAGGTGTAAACCGGGCAAAGTTCAGGTGTGTTGGTCTGCCGGGCGTAT 250
68 yAlaGlyValLysProGlyLysValProGlyValGlyLeuProGlyVal 84
251 ACCCGGGTTTCGGTGTCTGTTCCGGGCGCGCGTTTCCAGGTGTTGGTGT 300
85 yrProGlyPheGlyAlaValProGlyAlaArgPheProGlyValGlyVal 100
301 CTGCCGGGCGTTCCGACCGGTGCAGGTGTAAACCGAAGGCACCAGGTGT 350
101 LeuProGlyValProThrGlyAlaGlyValLysProLysAlaProGlyVa 117
351 AGGCGGGCGGTTCGCGGGTATCCCGGGTGTGGCCCGTTCGGTGGTCCGC 400
118 lGlyGlyAlaPheAlaGlyIleProGlyValGlyProPheGlyGlyProG 134
401 AGCCAGGCGTTCCGCTGGGTACCCGATCAAAGCGCGAAGCTTCCAGGT 450
135 lnProGlyValProLeuGlyTyrProIleLysAlaProLysLeuProGly 150
451 GGCTACGGTCTGCCGTACACCACCGGTAAACTGCCGTACGGCTACGGTCC 500
151 GlyTyrGlyLeuProTyrThrThrGlyLysLeuProTyrGlyTyrGlyPr 167
501 GGGTGGCGTAGCAGGTGCTGCCGGTAAAGCAGGCTACCCAACCGGTACTG 550
168 oGlyGlyValAlaGlyAlaAlaGlyLysAlaGlyTyrProThrGlyThrG 184
551 GTGTTGGTCCGCAGGCTGCTGCCGCAGCTGCCGGAAGGCAGCAGCAAAA 600
185 lyValGlyProGlnAlaAlaAlaAlaAlaAlaAlaLysAlaAlaAlaLys 200
601 TTCGGCGCGGGTGCAGCGGGTTTCGGTGTCTGTTCCGGGCGTAGGTGGTGC 650
201 PheGlyAlaGlyAlaAlaGlyPheGlyAlaValProGlyValGlyGlyAl 217
651 TGGCGTTCCGGGTGTTCCAGGTGCGATCCCGGCATCGGTGGTATCCGAG 700
218 aGlyValProGlyValProGlyAlaIleProGlyIleGlyGlyIleAlaG 234
701 GCGTAGGTACTCCGGCGGGCGGCTGCCGGCTGCCGCAGCTGCCGGAAGCA 750
235 lyValGlyThrProAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaLysAla 250

Figure 3(1)

751 GCTAAATACGGTGCAGCAGGCCTGGTTCGGGGTGGTCCAGGCTTCGG 800
|||
251 AlaLysTyrGlyAlaAlaAlaGlyLeuValProGlyGlyProGlyPheG 267
801 TCCGGGTGTGTAGGCGTTCCGGGTTTCGGTGTCTGTTCGGGGCGTAGGT 850
|||
268 yProGlyValValGlyValProGlyPheGlyAlaValProGlyValGlyV 284
851 TTCCAGGTGCGGGCATCCCGTTGTACCGGGTGCAGGTATCCCGGGCGCT 900
|||
285 alProGlyAlaGlyIleProValValProGlyAlaGlyIleProGlyAla 300
901 GCGGGTTTCGGTGTCTGTATCCCGGAAGCGGCAGCTAAGGCTGTGCGAA 950
|||
301 AlaGlyPheGlyAlaValSerProGluAlaAlaAlaLysAlaAlaAlaLy 317
951 AGCTGCGAAATACGGAGCTCGTCCGGGGCGTGGTGTGGTGGCATCCCGA 1000
|||
318 sAlaAlaLysTyrGlyAlaArgProGlyValGlyValGlyGlyIleProT 334
1001 CCTACGGTGTAGGTGCAGGCGGTTTCCAGGTTTCGGCGTGGTGTGTGGT 1050
|||
335 hrTyrGlyValGlyAlaGlyGlyPheProGlyPheGlyValGlyValGly 350
1051 GGCATCCCGGGTGTAGCTGGTGTTCGGTCTGTGGTGGCGTACCGGGTGT 1100
|||
351 GlyIleProGlyValAlaGlyValProSerValGlyGlyValProGlyVa 367
1101 TGGTGGCGTTCAGGTGTAGGTATCTCCCGGAAGCGCAGGCAGCTGCGG 1150
|||
368 lGlyGlyValProGlyValGlyIleSerProGluAlaGlnAlaAlaAlaA 384
1151 CAGCTAAGCAGCGAAGTACGGCGTTGGTACTCCGGCGGCAGCAGCTGCT 1200
|||
385 laAlaLysAlaAlaLysTyrGlyValGlyThrProAlaAlaAlaAlaAla 400
1201 AAAGCAGCGGCTAAGCAGCGCAGTTCCGACTAGTTCCGGGGCGTAGGTGT 1250
|||
401 LysAlaAlaAlaLysAlaAlaGlnPheGlyLeuValProGlyValGlyVa 417
1251 TGCGCCAGGTGTGGCGTAGCACCGGGTGTGGTGTGTGCTCCGGGGCGTAG 1300
|||
418 lAlaProGlyValGlyValAlaProGlyValGlyValAlaProGlyValG 434
1301 GTCTGGCACCGGGTGTGGCGTTGCACCAGGTGTAGGTGTTCGGCGGGGC 1350
|||
435 lyLeuAlaProGlyValGlyValAlaProGlyValGlyValAlaProGly 450
1351 GTTGGTGTAGCACCGGGTATCCGGTCCGGGTGGCGTTTCGGGCTGTGCGAA 1400
|||
451 ValGlyValAlaProGlyIleGlyProGlyGlyValAlaAlaAlaAlaLy 467
1401 ATCTGCTGCGAAGGTGTCTGCGAAGCGCAGCTGCGTGCAGCAGCTGGTC 1450
|||
468 sSerAlaAlaLysValAlaAlaLysAlaGlnLeuArgAlaAlaAlaGlyL 484
1451 TGGGTGCGGGCATCCCGGTTCTGGGTGTAGGTGTGGTGTTCGGGGCGCT 1500
|||
485 euGlyAlaGlyIleProGlyLeuGlyValGlyValGlyValProGlyLeu 500

Figure 3(2)

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1501 GGTGTAGGTGCAGGGGTACCGGGCCTGGGTGTGGTGCAGGCGTTCCGGG 1550
|||
501 GlyValGlyAlaGlyValProGlyLeuGlyValGlyAlaGlyValProGly 517
1551 TTTCGGTGCCTGTTCCGGGGCGCGCTGGCTGCTGCGAAGCGGCGAATACG 1600
|||
518 yPheGlyAlaValProGlyAlaLeuAlaAlaAlaLysAlaAlaLysTyrG 534
1601 GTGCTGTTCGGGTGTACTGGGCGGTCTGGGTGCTCTGGGCGGTGTGGT 1650
|||
535 lyAlaValProGlyValLeuGlyGlyLeuGlyAlaLeuGlyGlyValGly 550
1651 ATCCCGGGCGGTGTGTAGGTGCAGGCCAGCTGCAGCTGCTGCTGCGGC 1700
|||
551 IleProGlyGlyValValGlyAlaGlyProAlaAlaAlaAlaAlaAla 567
1701 AAAGGCAGCGGCGAAGCAGCTCAGTTCTGGTCTGGTGGTGCAGCAGGT 1750
|||
568 aLysAlaAlaAlaLysAlaAlaGlnPheGlyLeuValGlyAlaAlaGlyL 584
1751 TGGGCGGTCTGGGTGTGGCGGTCTGGGTGTACCGGGCGGTGGTGGTCTG 1800
|||
585 euGlyGlyLeuGlyValGlyGlyLeuGlyValProGlyValGlyGlyLeu 600
1801 GGTGGCATCCCGCGGGCGGCGGCAGCTAAAGCGGCTAAATACGGTGCAGC 1850
|||
601 GlyGlyIleProProAlaAlaAlaAlaLysAlaAlaLysTyrGlyAlaAl 617
1851 AGGTCGTGGGTGGCGTTCTGGGTGGTGTCTGGTTCAGTTCCCACTGGGCGGTG 1900
|||
618 aGlyLeuGlyGlyValLeuGlyGlyAlaGlyGlnPheProLeuGlyGlyV 634
1901 TAGCGGCAGTCCGGGTTTCTGGTCTGTCCCGATCTTCCAGGCGGTGCA 1950
|||
635 alAlaAlaArgProGlyPheGlyLeuSerProIlePheProGlyGlyAla 650
1951 TGCTGTGGGTAAAGCTTGCGGCCGTAAACGTAAA 1983
|||
651 CysLeuGlyLysAlaCysGlyArgLysArgLys 661

Figure 3(3)

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1 ATGGGTGGCGTTCCGGGTGCTGTTCCGGGTGGCGTTCCGGGTGGTGTATT 50
|||
1 ATGGGTGGCGTTCCGGGTGCTATCCCGGTGGCGTTCCGGGTGGTGTATT 50
51 CTACCCAGGCGCGGGTTCGGTGC..... 74
|||
51 CTACCCAGGCGCGGGTCTGGGTGCACTGGGCGGTGGTGCCTGGGCCCGG 100
:
:
75TGT 77
|||
151 GGTGCAGGTCTGGGCGCGTTCCCGGCGGTACCTTCCCGGTGCTCTGGT 200
|||
78 TCCGGGTGGCGTTGCAGACG CAGCTGCTGCGTACAAAGCGGCAAAGGCAG 127
|||
201 TCCGGGTGGCGTTGCAGACG CAGCTGCTGCGTACAAAGCGGCAAAGGCAG 250
|||
128 GTGCGGGTCTGGGCGGGGTACCAGGTGTGGCGGTCTGGGTGTATCTGCT 177
|||
251 GTGCGGGTCTGGGCGGGGTACCAGGTGTGGCGGTCTGGGTGTATCTGCT 300
|||
178 GGCGCAGTTGTTCCGCAGCCGGGTGCAGGTGTAAACCGGGCAAAGTTCC 227
|||
301 GGCGCAGTTGTTCCGCAGCCGGGTGCAGGTGTAAACCGGGCAAAGTTCC 350
|||
228 AGGTGTTGGTCTGCGGGCGTATACCGGGTTTCGGTGTCTGTTCCGGGCG 277
|||
351 AGGTGTTGGTCTGCGGGCGTATACCGGGT...GGTGTCTGCGGGCG 397
|||
278 CGCGTTTCCAGGTGTTGGTGTACTGCGGGCGTTCCGACCGGTGCAGGT 327
|||
398 CGCGTTTCCAGGTGTTGGTGTACTGCGGGCGTTCCGACCGGTGCAGGT 447
|||
328 GTTAAACCGAAGGCACCAGGTGTAGGCGGCGGTTCCGCGGTATCCCGGG 377
|||
448 GTTAAACCGAAGGCACCAGGTGTAGGCGGCGGTTCCGCGGTATCCCGGG 497
|||
378 TGTGGGCCCGTTCCGTGGTCCGCAGCCAGGCGTTCCGCTGGGTACCCGA 427
|||
498 TGTGGGCCCGTTCCGTGGTCCGCAGCCAGGCGTTCCGCTGGGTACCCGA 547
|||
428 TCAAAGCGCCGAAGCTTCCAGGTGGCTACGCTCTGCGGTACACCACCGGT 477
|||
548 TCAAAGCGCCGAAGCTTCCAGGTGGCTACGCTCTGCGGTACACCACCGGT 597
|||
478 AAACCTGCCGTACGGCTACGGTCCGGGTGGCGTAGCAGGTGCTGCGGGTAA 527
|||
598 AAACCTGCCGTACGGCTACGGTCCGGGTGGCGTAGCAGGTGCTGCGGGTAA 647
|||
528 AGCAGGCTACCCAACCGGTACTGGTGTGGTCCGCAGGCTGCTGCGGCAG 577
|||
648 AGCAGGCTACCCAACCGGTACTGGTGTGGTCCGCAGGCTGCTGCGGCAG 697
|||
578 CTGCGGCGAAGGCAGCAGCAAATTCGGCGCGGGTGCAGCGGTTTCGGT 627
|||
698 CTGCGGCGAAGGCAGCAGCAAATTCGGCGCGGGTGCAGCG.....GGT 741
|||
628 GCTGTTCCGGGCGTAGGTGGTGTGGCGTTCGGGTGTTCCAGGTGCGAT 677
|||
742 GTTCTGCGGGCGTAGGTGGTGTGGCGTTCGGGTGTTCCAGGTGCGAT 791

Figure 4(1)

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678 CCGGGGCATCGGTGGTATCGCAGGCGTAGGTACTCCGGCGGGCCGCTGCGG 727
|||
792 CCCGGGCATCGGTGGTATCGCAGGCGTAGGTACTCCGGCGGGCCGCTGCGG 841
|||
728 CTGCGGCAGCTGCGGCGAAGCAGCTAAATAAGGTGCGGCAGCAGGCCTG 777
|||
842 CTGCGGCAGCTGCGGCGAAGCAGCTAAATAAGGTGCGGCAGCAGGCCTG 891
|||
778 GTTCGGGGTGGTCCAGGCTTCGGTCCGGGTGTTGTAGGCGTTCCGGGTTT 827
|||
892 GTTCGGGGTGGTCCAGGCTTCGGTCCGGGTGTTGTAGGCGTTCCGGGTT.. 939
|||
828 CGGTGCTGTTCCGGGCGTAGGTGTTCCAGGTGCGGGCATCCCGTTGTAC 877
|||
940 .GCTGGTGTTCGGGCGTAGGTGTTCCAGGTGCGGGCATCCCGTTGTAC 988
|||
878 CGGGTGCAAGTATCCCGGGCGCTGCGGGTTTCGGTGCTGTATCCCGGAA 927
|||
989 CGGGTGCAAGTATCCCGGGCGCTGCGGGTTTCAGGTGTGTATCCCGGAA 1038
|||
928 GCGGCAGCTAAGGCTGCTGCGAAGCTGCGAATAAGGAGCTCGTCCGGG 977
|||
1039 GCGGCAGCTAAGGCTGCTGCGAAGCTGCGAATAAGGAGCTCGTCCGGG 1088
|||
978 CGTTGGTGTGGTGGCATCCCGACCTACGGTGTAGGTGCAGGCGGTTTC 1027
|||
1089 CGTTGGTGTGGTGGCATCCCGACCTACGGTGTAGGTGCAGGCGGTTTC 1138
|||
1028 CAGGTTTCGGCGTTGGTGTGGTGGCATCCCGGGTGTAGCTGGTGTTCG 1077
|||
1139 CAGGTTTCGGCGTTGGTGTGGTGGCATCCCGGGTGTAGCTGGTGTTCG 1188
|||
1078 TCTGTTGGTGGCGTACCGGGTGTGGTGGCGTTCCAGGTGTAGGTATCTC 1127
|||
1189 TCTGTTGGTGGCGTACCGGGTGTGGTGGCGTTCCAGGTGTAGGTATCTC 1238
|||
1128 CCCGGAAGCGCAGGCAGCTGCGGCAGCTAAAGCAGCGAAGTACGGCGTTG 1177
|||
1239 CCCGGAAGCGCAGGCAGCTGCGGCAGCTAAAGCAGCGAAGTACGGCGTTG 1288
|||
1178 GTACTCCGGCGGCAGCAGCTGCTAAAGCAGCGGCTAAAGCAGCGCAGTTC 1227
|||
1289 GTACTCCGGCGGCAGCAGCTGCTAAAGCAGCGGCTAAAGCAGCGCAGTTC 1338
|||
1228 GGACTAGTTCCGGGCGTAGGTGTTGCGCCAGGTGTTGGCGTAGCACCGGG 1277
|||
1339 GGACTAGTTCCGGGCGTAGGTGTTGCGCCAGGTGTTGGCGTAGCACCGGG 1388
|||
1278 TGTGGGTGTGCTCCGGGCGTAGGTCTGGCACCGGGTGTGGCGTTGCAC 1327
|||
1389 TGTGGGTGTGCTCCGGGCGTAGGTCTGGCACCGGGTGTGGCGTTGCAC 1438
|||
1328 CAGGTGTAGGTGTGCGCCGGCGGTGGTGTAGCACCGGGTATCGGTCCG 1377
|||
1439 CAGGTGTAGGTGTGCGCCGGCGGTGGTGTAGCACCGGGTATCGGTCCG 1488
|||
1378 GGTGGCGTTGCGGCTGCTGCGAATCTGCTGCGAAGGTTGCTGCGAAGC 1427
|||
1489 GGTGGCGTTGCGGCTGCTGCGAATCTGCTGCGAAGGTTGCTGCGAAGC 1538
|||

Figure 4(2)

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1428 GCAGCTGCGTGCAGCAGCTGGTCTGGGTGCGGGCATCCCAGGTCTGGGTG 1477
1539 GCAGCTGCGTGCAGCAGCTGGTCTGGGTGCGGGCATCCCAGGTCTGGGTG 1588
1478 TAGGTGTTGGTGTTCGGGCTGGGTGTAGGTGCAGGGGTACCGGGCCTG 1527
1589 TAGGTGTTGGTGTTCGGGCTGGGTGTAGGTGCAGGGGTACCGGGCCTG 1638
1528 GGTGTTGGTGCAGGCGTTCCGGGTTTCGGTGC..... 1559
1639 GGTGTTGGTGCAGGCGTTCCGGGTTTCGGTGCCTGGGCGGACGAAGGTGT 1688
:
:
1560TGTTCCGGGCGCGCTGGCT 1578
1739 AGCACCTGCCGTCTACCCCGTCTCTCCACGTGTTCCGGGCGCGCTGGCT 1788
1579 GCTGCGAAAGCGGCGAAATACGGT...GCTGTTCCGGGTGTACTGGGCGG 1625
1789 GCTGCGAAAGCGGCGAAATACGGTGCAGCGGTTCGGGTGTACTGGGCGG 1838
1626 TCTGGGTGCTCTGGGCGGTGTGTGATCCCGGCGGTGTGTAGGTGCAG 1675
1839 TCTGGGTGCTCTGGGCGGTGTGTGATCCCGGCGGTGTGTAGGTGCAG 1888
1676 GCCCAGCTGCAGCTGCTGCTGCGGCAAGGCAGCGGCGAAAGCAGCTCAG 1725
1889 GCCCAGCTGCAGCTGCTGCTGCGGCAAGGCAGCGGCGAAAGCAGCTCAG 1938
1726 TTCGGTCTGGTTGGTGCAGCAGGTCTGGGCGGTCTGGGTGTGGCGGTCT 1775
1939 TTCGGTCTGGTTGGTGCAGCAGGTCTGGGCGGTCTGGGTGTGGCGGTCT 1988
1776 GGGTGTACCGGGCGTTGGTGGTCTGGGTGGCATCCCGCGGCGGCGGCAG 1825
1989 GGGTGTACCGGGCGTTGGTGGTCTGGGTGGCATCCCGCGGCGGCGGCAG 2038
1826 CTAAAGCGGCTAAATACGGTGCAGCAGGTCTGGGTGGCGTTCTGGGTGGT 1875
2039 CTAAAGCGGCTAAATACGGTGCAGCAGGTCTGGGTGGCGTTCTGGGTGGT 2088
1876 GCTGGTCACTTCCCACTGGGCGGTGTAGCGGCACGTCCGGGTTTCGGTCT 1925
2089 GCTGGTCACTTCCCACTGGGCGGTGTAGCGGCACGTCCGGGTTTCGGTCT 2138
1926 GTCCCGATCTTCCCAAGGCGGTGCATGCCTGGGTAAAGCTTGGCGGCGTA 1975
2139 GTCCCGATCTTCCCAAGGCGGTGCATGCCTGGGTAAAGCTTGGCGGCGTA 2188
1976 AACGTAAATAATGATAG 1992
2189 AACGTAAATAATGATAG 2205

Figure 4(3)

Figure 5(1)

Figure 5(2)

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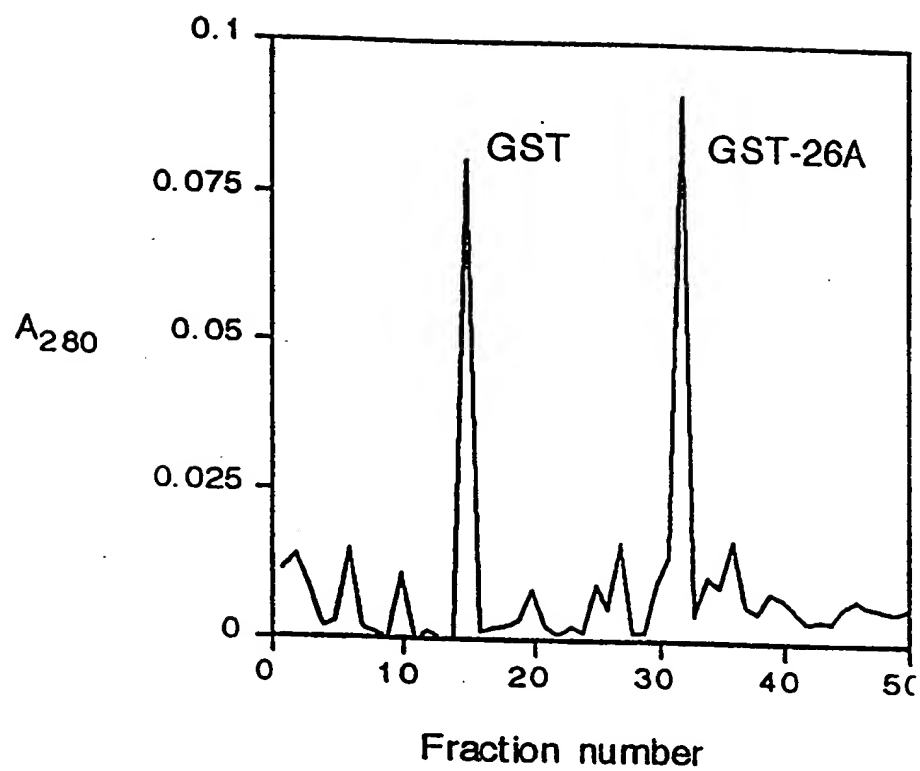


Fig. 6(a)

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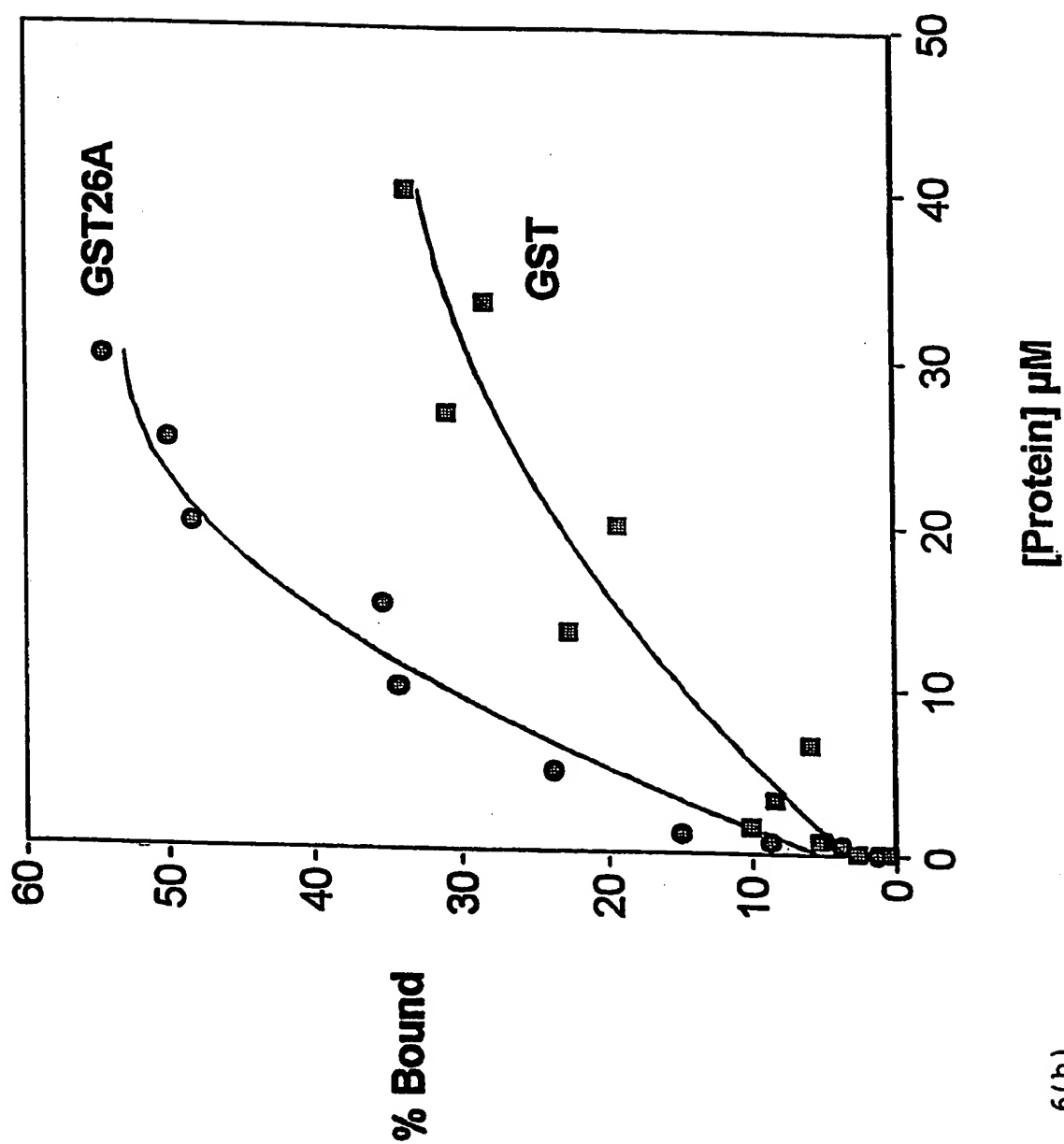


Fig. 6(b)

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948 TCCGCCATGGGAGGTGTTCGGGCGCGCTGGCTGCTGCGAAAGCGGCGAA 997
||||||||||||||||||||||||||||||||||||||||||
1 SerAlaMetGlyGlyValProGlyAlaLeuAlaAlaLysAlaAlaLys 17

998 ATACGGGTGCAGCGGTTCCGGGTGTACTGGGCGGTCTGGGTGCTCTGGGCG 1047
||||||||||||||||||||||||||||||||||||||||||
18 sTyrGlyAlaAlaValProGlyValLeuGlyGlyLeuGlyAlaLeuGlyG 34

1048 GTGTTGGTATCCCGGGCGGTGTTGTAGGTGCAGGCCAGCTGCAGCTGCT 1097
||||||||||||||||||||||||||||||||||||||||||
35 lyValGlyIleProGlyGlyValValGlyAlaGlyProAlaAlaAlaAla 50

1098 GCTGCGGCAAAGGCAGCGGCGAAAGCAGCTCAGTTCGGTCTGGTTGGTGC 1147
||||||||||||||||||||||||||||||||||||||||||
51 AlaAlaAlaLysAlaAlaAlaLysAlaAlaGlnPheGlyLeuValGlyAl 67

1148 AGCAGGTCTGGGCGGTCTGGGTGTTGGCGGTCTGGGTGTACCGGGCGTTG 1197
||||||||||||||||||||||||||||||||||||||||||
68 aAlaGlyLeuGlyGlyLeuGlyValGlyGlyLeuGlyValProGlyValG 84

1198 GTGGTCTGGGTGGCATCCCGCCGGCGGCGGCAGCTAAAGCGGCTAAATAC 1247
||||||||||||||||||||||||||||||||||||||||||
85 lyGlyLeuGlyGlyIleProProAlaAlaAlaAlaLysAlaAlaLysTyr 100

1248 GGTGCAGCAGGTCTGGGTGGCGTTCTGGGTGGTGCTGGTCAGTTCCCACT 1297
||||||||||||||||||||||||||||||||||||||||||
101 GlyAlaAlaGlyLeuGlyGlyValLeuGlyGlyAlaGlyGlnPheProLe 117

1298 GGGCGGTGTAGCGGCACGTCCGGGTTTCGGTCTGTCCCCGATCTTCCCAG 1347
||||||||||||||||||||||||||||||||||||||||||
118 uGlyGlyValAlaAlaArgProGlyPheGlyLeuSerProIlePheProG 134

1348 GCGGTGCATGCCTGGGTAAAGCTTGCGGCCGTAAACGTAAA 1388
||||||||||||||||||||||||||||||||||||||||||
135 lyGlyAlaCysLeuGlyLysAlaCysGlyArgLysArgLys 147

Figure 7

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948 TCCGCCATGGGAGCTCTGGTAGGCCTGGGCGTACCGGGCCTGGGTGTTGG 997
|||||
1 SerAlaMetGlyAlaLeuValGlyLeuGlyValProGlyLeuGlyValGl 17

998 TGCAGGCGTTCCGGGTTTCGGTGCTGGCGCGGACGAAGGTGTACGTCGTT 1047
|||||
18 yAlaGlyValProGlyPheGlyAlaGlyAlaAspGluGlyValArgArgS 34

1048 CCCTGTCTCCAGAACTGCGTGAAGGTGACCCGTCCTCTTCCCAGCACCTG 1097
|||||
35 erLeuSerProGluLeuArgGluGlyAspProSerSerSerGlnHisLeu 50

1098 CCGTCTACCCCGTCCTCTCCACGTGTTCCGGGCGCGCTGGCTGCTGCGAA 1147
|||||
51 ProSerThrProSerSerProArgValProGlyAlaLeuAlaAlaAlaLy 67

1148 AGCGGCGAAATACGGTGCGAGCGGTTCCGGGTGTACTGGGCGGTCTGGGTG 1197
|||||
68 sAlaAlaLysTyrGlyAlaAlaValProGlyValLeuGlyGlyLeuGlyA 84

1198 CTCTGGGCGGTGTTGGTATCCCGGGCGGTGTTGTAGGTGCAGGCCAGCT 1247
|||||
85 laLeuGlyGlyValGlyIleProGlyGlyValValGlyAlaGlyProAla 100

Figure 8(1)

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1248 GCAGCTGCTGCTGCGGCAAAGGCAGCGGCGAAAGCAGCTCAGTTCGGTCT 1297
|||||
101 AlaAlaAlaAlaAlaAlaLysAlaAlaAlaLysAlaAlaGlnPheGlyLe 117
.
1298 GGTGGTGCAGCAGGTCTGGGCGGTCTGGGTGTTGGCGGTCTGGGTGTAC 1347
|||||
118 uValGlyAlaAlaGlyLeuGlyGlyLeuGlyValGlyGlyLeuGlyValP 134
.
1348 CGGGCGTTGGTGGTCTGGGTGGCATCCCGCCGGCGGCGGCAGCTAAAGCG 1397
|||||
135 roGlyValGlyGlyLeuGlyGlyIleProProAlaAlaAlaAlaLysAla 150
.
1398 GCTAAATACGGTGCAGCAGGTCTGGGTGGCGTTCTGGGTGGTGGTCA 1447
|||||
151 AlaLysTyrGlyAlaAlaGlyLeuGlyGlyValLeuGlyGlyAlaGlyGl 167
.
1448 GTTCCCACTGGGCGGTGTAGCGGCACGTCCGGGTTTCGGTCTGTCCCCGA 1497
|||||
168 nPheProLeuGlyGlyValAlaAlaArgProGlyPheGlyLeuSerProI 184
.
1498 TCTTCCCAGGCGGTGCATGCCTGGGTAAAGCTTGCGGCGGTAAACGTAAA 1547
|||||
185 lePheProGlyGlyAlaCysLeuGlyLysAlaCysGlyArgLysArgLys 200

Figure 8(2)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU 98/00564

A. CLASSIFICATION OF SUBJECT MATTER																						
Int Cl ⁶ : C07K 14/435, C07H 21/04, A61K 38/17, C12N 15/12, C12P 21/02																						
According to International Patent Classification (IPC) or to both national classification and IPC																						
B. FIELDS SEARCHED																						
Minimum documentation searched (classification system followed by classification symbols)																						
IPC C07K 14/435, C07H 21/04, A61K 38/17, C12N 15/12, C12P 21/02																						
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched																						
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)																						
ANGIS																						
C. DOCUMENTS CONSIDERED TO BE RELEVANT																						
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.																				
X	Proc. Natl. Acad. Sci. USA, Volume 84, issued August 1987, Z. Indik et al, "Alternative splicing of human elastin in RNA indicated by sequence analysis of cloned genomic and complementary DNA", pages 5680 to 5684 whole document	1-47, 50-65																				
X	Connective Tissue Research, Vol. 16, issued 1987, Z. Indik et al, "Structure of the 3' region of the human elastin gene : Great abundance of Alu Repetitive sequences and few coding sequences", pages 197 to 211 whole document	1-47, 50-65																				
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input type="checkbox"/> See patent family annex																						
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"P"	document published prior to the international filing date but later than the priority date claimed																					
Date of the actual completion of the international search 16 October 1998		Date of mailing of the international search report 22 OCT 1998																				
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929		Authorized officer Gavin Thompson Telephone No.: (02) 6283 2240																				

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU 98/00564

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Cell, Vol. 86, issued July 12 1996, J.M. Frangiskakis et al, "LIM-kinase 1 Hemizygosity Implicated in Impaired Visuospatial Constructive Cognition", pages 59 to 69 whole document	1-13, 18-29, 42-47, 50-62
X	Laboratory Investigation, Vol. 58, No. 3, issued 1988, M.J. Fazio et al, "Isolation and Characterization of Human Elastin cDNAs, and Age-Associated Variation in Elastin Gene Expression in Cultured Skin Fibroblasts", pages 270 to 277 whole document	1-13, 18-29, 38-47, 50-62
X	The Journal of Investigative Dermatology, Vol. 91, No. 5, issued November 1988, M.J. Fazio et al. "Cloning of Full-length Elastin cDNAs from a Human Skin Fibroblast Recombinant cDNA Library : Further Elucidation of Alternative Splicing Utilizing Exon-specific Oligonucleotides, pages 458 to 464 whole document	1-13, 18-29, 42-47, 50-62
X	Genomics, Vol. 36, issued 1996, L.R. Osborne et al, "Identification of Genes from a 500 kb Region at 7q11.23. That is commonly deleted in Williams Syndrome Patients", pages 328 to 336. whole document	1-5, 18-29, 42- 47, 50-62
X	The Journal of Biological Chemistry, Vol. 264, issued May 25 1989, M.M Bashir et al, "Characterization of the Complete Human Elastin Gene", pages 8887 to 8891 whole document	1-5, 10-13, 42-47, 50-62